GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 21, 2005, 02:55:41 ; Search time 546 Seconds
(without alignments)
170.537 Million cell updates/sec

Title: US-10-075-994A-1
Perfect score: 15
Sequence: 1 gtgctccattgatgc 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6054689 seqs, 3103772919 residues

Total number of hits satisfying chosen parameters: 12109378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
19: /cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
20: /cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq:*
21: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq:*
22: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
23: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
24: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
25: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	15	100.0	15	9	US-09-930-283A-1	Sequence 1, Appli
c	2	15	100.0	15	9	US-09-930-283A-3	Sequence 3, Appli
	3	15	100.0	15	10	US-09-895-480A-15	Sequence 15, Appl
	4	15	100.0	15	15	US-10-290-545-25	Sequence 25, Appl
	5	15	100.0	15	16	US-10-365-623-16	Sequence 16, Appl
	6	15	100.0	15	17	US-10-075-994A-1	Sequence 1, Appli
c	7	15	100.0	15	17	US-10-075-994A-3	Sequence 3, Appli
	8	15	100.0	15	17	US-10-075-994A-4	Sequence 4, Appli
	9	15	100.0	15	17	US-10-347-924-1	Sequence 1, Appli
	10	15	100.0	15	17	US-10-437-263-25	Sequence 25, Appl
	11	15	100.0	15	17	US-10-437-275-25	Sequence 25, Appl
	12	15	100.0	15	17	US-10-437-258-25	Sequence 25, Appl
	13	15	100.0	15	21	US-10-925-734-15	Sequence 15, Appl
	14	15	100.0	20	14	US-10-057-550-49	Sequence 49, Appl
	15	15	100.0	20	15	US-10-173-225B-47	Sequence 47, Appl
	16	15	100.0	25	9	US-09-930-283A-2	Sequence 2, Appli
	17	15	100.0	25	17	US-10-075-994A-2	Sequence 2, Appli
c	18	15	100.0	25	21	US-10-809-189-113549	Sequence 113549,
c	19	15	100.0	25	21	US-10-809-189-113550	Sequence 113550,
c	20	15	100.0	165	9	US-09-728-446-1067	Sequence 1067, Ap
c	21	15	100.0	478	10	US-09-918-995-4443	Sequence 4443, Ap
	22	15	100.0	597	16	US-10-029-386-10799	Sequence 10799, A
c	23	15	100.0	673	13	US-10-027-632-244006	Sequence 244006,
c	24	15	100.0	673	13	US-10-027-632-244007	Sequence 244007,
c	25	15	100.0	673	17	US-10-027-632-244006	Sequence 244006,
c	26	15	100.0	673	17	US-10-027-632-244007	Sequence 244007,
	27	15	100.0	968	19	US-10-767-795-1291	Sequence 1291, Ap
	28	15	100.0	1161	19	US-10-437-963-36158	Sequence 36158, A
c	29	15	100.0	2975	16	US-10-440-341-2	Sequence 2, Appli
c	30	15	100.0	2977	9	US-09-969-347-207	Sequence 207, App
c	31	15	100.0	2977	10	US-09-963-131-159	Sequence 159, App
c	32	15	100.0	2977	14	US-10-057-550-25	Sequence 25, Appl
c	33	15	100.0	2977	15	US-10-173-225B-64	Sequence 64, Appl
c	34	15	100.0	2977	16	US-10-371-138-1	Sequence 1, Appli
c	35	15	100.0	2977	21	US-10-843-641A-8336	Sequence 8336, Ap
c	36	15	100.0	2977	21	US-10-936-273-29	Sequence 29, Appl
c	37	15	100.0	3228	21	US-10-926-543-44	Sequence 44, Appl
c	38	15	100.0	76698	21	US-10-936-273-30	Sequence 30, Appl
c	39	14	93.3	25	21	US-10-809-189-113548	Sequence 113548,
	40	14	93.3	223	11	US-09-732-627A-2120	Sequence 2120, Ap
c	41	14	93.3	225	19	US-10-437-963-4788	Sequence 4788, Ap
c	42	14	93.3	327	9	US-09-983-965-3423	Sequence 3423, Ap
	43	14	93.3	406	20	US-10-425-115-149033	Sequence 149033,
	44	14	93.3	475	18	US-10-424-599-103047	Sequence 103047,
	45	14	93.3	602	20	US-10-357-930-50238	Sequence 50238, A

ALIGNMENTS

RESULT 1
US-09-930-283A-1
; Sequence 1, Application US/09930283A
; Patent No. US20020160038A1
; GENERAL INFORMATION:
; APPLICANT: Kasid, Usha
; Gokhale, Prafulla
; Dritschilo, Anatoly
; Rahman, Aqulur
; TITLE OF INVENTION: Liposomes contaiing Oligonucelotides
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hendricks and Assoc.
; STREET: P.O. Box 2509
; CITY: Fairfax
; STATE: VA
; COUNTRY: US
; ZIP: 22031
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/930,283A
; FILING DATE: 16-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/354,109
; FILING DATE: 1999-07-15

```
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Hendricks, Glenna
;            REGISTRATION NUMBER: 32,535
;            REFERENCE/DOCKET NUMBER: kasid
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (703) 591-4470
;            TELEFAX: (703) 591-4428
;   INFORMATION FOR SEQ ID NO: 1:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 15 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: unknown
;       MOLECULE TYPE: DNA (genomic)
;       HYPOTHETICAL: NO
;       ANTI-SENSE: YES
;       SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-930-283A-1

  Query Match             100.0%;  Score 15;  DB 9;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATGC 15
              |||||||||||||||
Db          1 GTGCTCCATTGATGC 15


RESULT 2
US-09-930-283A-3/c
; Sequence 3, Application US/09930283A
; Patent No. US20020160038A1
;   GENERAL INFORMATION:
;       APPLICANT: Kasid, Usha
;                  Gokhale, Prafulla
;                  Dritschilo, Anatoly
;                  Rahman, Aqulur
;       TITLE OF INVENTION: Liposomes contaiing Oligonucelotides
;       NUMBER OF SEQUENCES: 3
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Hendricks and Assoc.
;            STREET: P.O. Box 2509
;            CITY: Fairfax
;            STATE: VA
;            COUNTRY: US
;            ZIP: 22031
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/930,283A
;            FILING DATE: 16-Aug-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/354,109
;            FILING DATE: 1999-07-15
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Hendricks, Glenna
;            REGISTRATION NUMBER: 32,535
;            REFERENCE/DOCKET NUMBER: kasid
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (703) 591-4470
;            TELEFAX: (703) 591-4428
;   INFORMATION FOR SEQ ID NO: 3:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 15 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: unknown
;       MOLECULE TYPE: DNA (genomic)
;       HYPOTHETICAL: NO
;       ANTI-SENSE: YES
;       SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-930-283A-3

  Query Match             100.0%;  Score 15;  DB 9;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATGC 15
              |||||||||||||||
Db         15 GTGCTCCATTGATGC 1


RESULT 3
US-09-895-480A-15
; Sequence 15, Application US/09895480A
; Publication No. US20030129221A1
;   GENERAL INFORMATION:
;       APPLICANT: Inex Pharmaceuticals Inc.
;       TITLE OF INVENTION: High Efficiency Encapsulation of Charged Therapeutic
;                           Agents in
;                           Lipid Vesicles
;       NUMBER OF SEQUENCES: 17
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Oppedahl & Larson LLP
;            STREET: PO Box 5068
;            CITY: Dillon
;            STATE: CO
;            COUNTRY: US
;            ZIP: 80435
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
;            COMPUTER: IBM Compatible
;            OPERATING SYSTEM: DOS 5.0
;            SOFTWARE: Word Perfect
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/895,480A
;            FILING DATE: 29-Jun-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: <Unknown>
;            FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: <Unknown>
;            REGISTRATION NUMBER: <Unknown>
;            REFERENCE/DOCKET NUMBER: <Unknown>
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: <Unknown>
;            TELEFAX: <Unknown>
;            TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 15:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 15
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: other nucleic acid
;       HYPOTHETICAL: no
;       ANTI-SENSE: yes
;       SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-895-480A-15

  Query Match             100.0%;  Score 15;  DB 10;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATGC 15
              |||||||||||||||
Db          1 GTGCTCCATTGATGC 15


RESULT 4
US-10-290-545-25
```

; Sequence 25, Application US/10290545
; Publication No. US20030125292A1
; GENERAL INFORMATION:
; APPLICANT: Semple, Sean
; APPLICANT: Klimuk, Sandy
; APPLICANT: Yuan, Zuan-Ning
; TITLE OF INVENTION: Improved Mucosal Vaccines and Methods for Using the Same
; FILE REFERENCE: A-71854/TAL/AXG
; CURRENT APPLICATION NUMBER: US/10/290,545
; CURRENT FILING DATE: 2002-11-07
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-290-545-25

Query Match 100.0%; Score 15; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCTCCATTGATGC 15
||||||||||||||||
Db 1 GTGCTCCATTGATGC 15

RESULT 5
US-10-365-623-16
; Sequence 16, Application US/10365623
; Publication No. US20030166512A1
; GENERAL INFORMATION:
; APPLICANT: Xie, Dong
; TITLE OF INVENTION: Protein Carrier System for Therapeutic Oligonucleotides
; FILE REFERENCE: 63024.000001
; CURRENT APPLICATION NUMBER: US/10/365,623
; CURRENT FILING DATE: 2003-02-13
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense oligonucleotide directed against human c-raf-1 protein
; OTHER INFORMATION: kinase
US-10-365-623-16

Query Match 100.0%; Score 15; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCTCCATTGATGC 15
||||||||||||||||
Db 1 GTGCTCCATTGATGC 15

RESULT 6
US-10-075-994A-1
; Sequence 1, Application US/10075994A
; Publication No. US20030215489A1
; GENERAL INFORMATION:
; APPLICANT: KASID, Usha
; APPLICANT: GOKHALE, Prafulla
; APPLICANT: PIE, Jin
; APPLICANT: MEWANI, Rajshree
; APPLICANT: AHMAD, Imran
; APPLICANT: DRITSCHILO, Anatoly
; APPLICANT: RAHMAN, Aquilur
; TITLE OF INVENTION: CHEMOSENSITIZING WITH LIPOSOMES CONTAINING OLIGONUCLEOTIDES
; FILE REFERENCE: 219604
; CURRENT APPLICATION NUMBER: US/10/075,994A
; CURRENT FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-075-994A-1

Query Match 100.0%; Score 15; DB 17; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCTCCATTGATGC 15
||||||||||||||||
Db 1 GTGCTCCATTGATGC 15

RESULT 7
US-10-075-994A-3/c
; Sequence 3, Application US/10075994A
; Publication No. US20030215489A1
; GENERAL INFORMATION:
; APPLICANT: KASID, Usha
; APPLICANT: GOKHALE, Prafulla
; APPLICANT: PIE, Jin
; APPLICANT: MEWANI, Rajshree
; APPLICANT: AHMAD, Imran
; APPLICANT: DRITSCHILO, Anatoly
; APPLICANT: RAHMAN, Aquilur
; TITLE OF INVENTION: CHEMOSENSITIZING WITH LIPOSOMES CONTAINING OLIGONUCLEOTIDES
; FILE REFERENCE: 219604
; CURRENT APPLICATION NUMBER: US/10/075,994A
; CURRENT FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-075-994A-3

Query Match 100.0%; Score 15; DB 17; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCTCCATTGATGC 15
||||||||||||||||
Db 15 GTGCTCCATTGATGC 1

RESULT 8
US-10-075-994A-4
; Sequence 4, Application US/10075994A
; Publication No. US20030215489A1
; GENERAL INFORMATION:
; APPLICANT: KASID, Usha
; APPLICANT: GOKHALE, Prafulla
; APPLICANT: PIE, Jin
; APPLICANT: MEWANI, Rajshree
; APPLICANT: AHMAD, Imran
; APPLICANT: DRITSCHILO, Anatoly
; APPLICANT: RAHMAN, Aquilur
; TITLE OF INVENTION: CHEMOSENSITIZING WITH LIPOSOMES CONTAINING OLIGONUCLEOTIDES
; FILE REFERENCE: 219604
; CURRENT APPLICATION NUMBER: US/10/075,994A
; CURRENT FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4

```
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic
US-10-075-994A-4

  Query Match             100.0%;  Score 15;  DB 17;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATGC 15
              |||||||||||||||
Db          1 GTGCTCCATTGATGC 15


RESULT 9
US-10-347-924-1
; Sequence 1, Application US/10347924
; Publication No. US20030229040A1
; GENERAL INFORMATION:
;  APPLICANT: Kasid, Usha
;  APPLICANT:  Gokhale, Prafulla
;  APPLICANT:  Zhang, Chuanbo
;  APPLICANT:  Dristschilo, Anatoly
;  APPLICANT:  Rahman, Aquilur
;  TITLE OF INVENTION: CATIONIC LIPOSOMAL DELIVERY SYSTEM AND THERAPEUTIC USE THEREOF
;  FILE REFERENCE: 220807
;  CURRENT APPLICATION NUMBER: US/10/347,924
;  CURRENT FILING DATE:  2003-01-21
;  PRIOR APPLICATION NUMBER: US 09/354,109
;  PRIOR FILING DATE: 1999-07-15
;  PRIOR APPLICATION NUMBER: US 08/957,327
;  PRIOR FILING DATE: 1997-10-24
;  PRIOR APPLICATION NUMBER: US 60/041,192
;  PRIOR FILING DATE: 1997-03-21
;  NUMBER OF SEQ ID NOS: 1
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide
US-10-347-924-1

  Query Match             100.0%;  Score 15;  DB 17;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATGC 15
              |||||||||||||||
Db          1 GTGCTCCATTGATGC 15


RESULT 10
US-10-437-263-25
; Sequence 25, Application US/10437263
; Publication No. US20040009943A1
; GENERAL INFORMATION:
;  APPLICANT: Semple, Sean
;  APPLICANT:  Tam, Ying K.
;  APPLICANT:  Chikh, Ghania
;  APPLICANT:  Hope, Michael J.
;  TITLE OF INVENTION: PATHOGEN VACCINES AND METHODS FOR USING THE SAME
;  FILE REFERENCE: A-72216/TAL
;  CURRENT APPLICATION NUMBER: US/10/437,263
;  CURRENT FILING DATE:  2003-05-12
;  PRIOR APPLICATION NUMBER: 60/379,343
;  PRIOR FILING DATE: 2002-05-10
;  PRIOR APPLICATION NUMBER: 60/460,646
;  PRIOR FILING DATE: 2003-04-04
;  PRIOR APPLICATION NUMBER: 60/454,298
;  PRIOR FILING DATE: 2003-03-12
;  NUMBER OF SEQ ID NOS: 34
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-437-263-25

  Query Match             100.0%;  Score 15;  DB 17;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATGC 15
              |||||||||||||||
Db          1 GTGCTCCATTGATGC 15


RESULT 11
US-10-437-275-25
; Sequence 25, Application US/10437275
; Publication No. US20040009944A1
; GENERAL INFORMATION:
;  APPLICANT: Tam, Ying K.
;  APPLICANT:  Semple, Sean
;  APPLICANT:  Klimuk, Sandra
;  APPLICANT:  Chikh, Ghania
;  TITLE OF INVENTION: METHYLATED IMMUNOSTIMULATORY OLIGONUCLEOTIDES AND METHODS OF
;  TITLE OF INVENTION:  USING THE SAME
;  FILE REFERENCE: A-72158/TAL
;  CURRENT APPLICATION NUMBER: US/10/437,275
;  CURRENT FILING DATE:  2003-05-12
;  PRIOR APPLICATION NUMBER: 60/379,343
;  PRIOR FILING DATE: 2002-05-10
;  PRIOR APPLICATION NUMBER: 60/460,646
;  PRIOR FILING DATE: 2003-04-04
;  PRIOR APPLICATION NUMBER: 10/290,545
;  PRIOR FILING DATE: 2002-11-07
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-437-275-25

  Query Match             100.0%;  Score 15;  DB 17;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATGC 15
              |||||||||||||||
Db          1 GTGCTCCATTGATGC 15


RESULT 12
US-10-437-258-25
; Sequence 25, Application US/10437258
; Publication No. US20040013649A1
; GENERAL INFORMATION:
;  APPLICANT: Tam, Ying K.
;  APPLICANT:  Semple, Sean
;  APPLICANT:  Klimuk, Sandra
;  APPLICANT:  Chikh, Ghania
;  TITLE OF INVENTION: CANCER VACCINES AND METHODS OF USING THE SAME
;  FILE REFERENCE: A-72252/TAL
;  CURRENT APPLICATION NUMBER: US/10/437,258
;  CURRENT FILING DATE:  2003-05-12
;  PRIOR APPLICATION NUMBER: 60/379,343
;  PRIOR FILING DATE: 2002-05-10
;  PRIOR APPLICATION NUMBER: 60/460,646
;  PRIOR FILING DATE: 2003-04-04
;  PRIOR APPLICATION NUMBER: 60/454,298
```

```
;  PRIOR FILING DATE: 2003-03-12
;  NUMBER OF SEQ ID NOS: 34
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25
;    LENGTH: 15
;    TYPE: DNA
;    ORGANISM: Homo sapiens
US-10-437-258-25

  Query Match             100.0%;  Score 15;  DB 17;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATGC 15
              |||||||||||||||
Db          1 GTGCTCCATTGATGC 15


RESULT 13
US-10-925-734-15
; Sequence 15, Application US/10925734
; Publication No. US20050008689A1
;   GENERAL INFORMATION:
;        APPLICANT: Inex Pharmaceuticals Inc.
;        TITLE OF INVENTION: High Efficiency Encapsulation of Charged
;                            Therapeutic
;                            Agents in
;                            Lipid Vesicles
;        NUMBER OF SEQUENCES: 17
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Oppedahl & Larson LLP
;             STREET: PO Box 5068
;             CITY: Dillon
;             STATE: CO
;             COUNTRY: US
;             ZIP: 80435
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS 5.0
;             SOFTWARE: Word Perfect
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/925,734
;             FILING DATE: 24-Aug-2004
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/895,480
;             FILING DATE: 29-Jun-2001
;        ATTORNEY/AGENT INFORMATION:
;             NAME: <Unknown>
;             REGISTRATION NUMBER: <Unknown>
;             REFERENCE/DOCKET NUMBER: <Unknown>
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: <Unknown>
;             TELEFAX: <Unknown>
;             TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 15:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 15
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: other nucleic acid
;        HYPOTHETICAL: no
;        ANTI-SENSE: yes
;        SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-10-925-734-15

  Query Match             100.0%;  Score 15;  DB 21;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATGC 15
              |||||||||||||||
Db          1 GTGCTCCATTGATGC 15


RESULT 14
US-10-057-550-49
; Sequence 49, Application US/10057550
; Publication No. US20030032607A1
; GENERAL INFORMATION:
;  APPLICANT: Monia, Brett P.
;  TITLE OF INVENTION: Antisense Oligonucleotide Modulation of raf Gene Expression
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/10/057,550
;  CURRENT FILING DATE:  2002-01-25
;  PRIOR APPLICATION NUMBER: 09/506,073
;  PRIOR FILING DATE: 2000-02-18
;  PRIOR APPLICATION NUMBER: US 09/143,214
;  PRIOR FILING DATE: 1998-08-28
;  PRIOR APPLICATION NUMBER: PCT/US98/13961
;  PRIOR FILING DATE: 1998-07-06
;  PRIOR APPLICATION NUMBER: US 08/888,982
;  PRIOR FILING DATE: 1997-07-07
;  PRIOR APPLICATION NUMBER: US 08/756,806
;  PRIOR FILING DATE: 1996-11-26
;  PRIOR APPLICATION NUMBER: PCT/US95/07111
;  PRIOR FILING DATE: 1995-05-31
;  PRIOR APPLICATION NUMBER: US 08/250,856
;  PRIOR FILING DATE: 1994-05-31
;  NUMBER OF SEQ ID NOS: 130
; SEQ ID NO 49
;    LENGTH: 20
;    TYPE: DNA
;    ORGANISM: artificial sequence
;    FEATURE:
;    OTHER INFORMATION: antisense sequence
US-10-057-550-49

  Query Match             100.0%;  Score 15;  DB 14;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATGC 15
              |||||||||||||||
Db          5 GTGCTCCATTGATGC 19


RESULT 15
US-10-173-225B-47
; Sequence 47, Application US/10173225B
; Publication No. US20030119769A1
; GENERAL INFORMATION:
;  APPLICANT: Monia, Brett P.
;  TITLE OF INVENTION: Antisense Oligonucleotide Modulation of raf Gene Expression
;  FILE REFERENCE: ISPH-0665
;  CURRENT APPLICATION NUMBER: US/10/173,225B
;  CURRENT FILING DATE:  2002-12-06
;  PRIOR APPLICATION NUMBER: US 10/057,550
;  PRIOR FILING DATE: 2002-01-25
;  PRIOR APPLICATION NUMBER: US 09/143,214
;  PRIOR FILING DATE: 1998-08-28
;  PRIOR APPLICATION NUMBER: PCT/US98/13961
;  PRIOR FILING DATE: 1998-07-06
;  PRIOR APPLICATION NUMBER: US 08/888,982
;  PRIOR FILING DATE: 1997-07-07
;  PRIOR APPLICATION NUMBER: US 08/756,806
;  PRIOR FILING DATE: 1996-11-26
;  PRIOR APPLICATION NUMBER: PCT/US95/07111
;  PRIOR FILING DATE: 1995-05-31
;  PRIOR APPLICATION NUMBER: US 08/250,856
;  PRIOR FILING DATE: 1994-05-31
;  NUMBER OF SEQ ID NOS: 109
; SEQ ID NO 47
;    LENGTH: 20
```

```
;   TYPE: DNA
;   ORGANISM: artificial sequence
;   FEATURE:
;   OTHER INFORMATION: antisense sequence
US-10-173-225B-47

  Query Match             100.0%;  Score 15;  DB 15;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATGC 15
              |||||||||||||||
Db          5 GTGCTCCATTGATGC 19


Search completed: June 21, 2005, 05:25:17
Job time : 549 secs
```

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: June 21, 2005, 03:49:31 ; Search time 427 Seconds
(without alignments)
207.953 Million cell updates/sec

Title: US-10-075-994A-1
Perfect score: 15
Sequence: 1 gtgctccattgatgc 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 4167226

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	15	100.0	15	2	AAV54043	Aav54043 Human ant
	2	15	100.0	15	2	AAV99435	Aav99435 Antisense
	3	15	100.0	15	3	AAZ98661	Aaz98661 Human c-r
	4	15	100.0	15	6	AAD22797	Aad22797 Human c-r
	5	15	100.0	15	9	ACC58517	Acc58517 Oligonucl
	6	15	100.0	15	9	ADA24233	Ada24233 Human c-r
c	7	15	100.0	15	10	ADB97458	Adb97458 Sense (AT
	8	15	100.0	15	10	ADB97456	Adb97456 Antisense
	9	15	100.0	15	10	ADF82830	Adf82830 Immunosti
	10	15	100.0	15	12	ADE90171	Ade90171 Human c-r
	11	15	100.0	15	12	ADE39690	Ade39690 Oligonucl
	12	15	100.0	15	12	ADF32025	Adf32025 Antisense
	13	15	100.0	15	12	ADF42926	Adf42926 Methylate
	14	15	100.0	15	12	ADL70154	Adl70154 Oligonucl
	15	15	100.0	15	13	ADR88950	Adr88950 Anti c-ra
	16	15	100.0	20	2	AAT27527	Aat27527 Mouse/rat
	17	15	100.0	20	2	AAZ11557	Aaz11557 Mouse and
	18	15	100.0	20	3	AAA73535	Aaa73535 Mouse and
	19	15	100.0	20	6	AAD44760	Aad44760 Mouse and
	20	15	100.0	20	10	ADF09751	Adf09751 Mouse/rat
	21	15	100.0	20	10	ACD42120	Acd42120 Antisense
	22	15	100.0	25	10	ADB97457	Adb97457 Oligo use
c	23	13	86.7	17	2	AAV90935	Aav90935 Human C-r
	24	13	86.7	20	2	AAT27482	Aat27482 Human c-r
	25	13	86.7	20	2	AAT59716	Aat59716 Human raf
	26	13	86.7	20	2	AAT62145	Aat62145 Human c-r
	27	13	86.7	20	2	AAZ11512	Aaz11512 Human c-r
	28	13	86.7	20	3	AAA73490	Aaa73490 Human c-r
	29	13	86.7	20	6	AAD44715	Aad44715 Human c-r
	30	13	86.7	20	10	ADF09706	Adf09706 Human c-r
	31	13	86.7	20	10	ACD42073	Acd42073 Antisense
c	32	12.4	82.7	20	2	AAX16555	Aax16555 Position
c	33	12.4	82.7	20	2	AAX16583	Aax16583 Position
c	34	12.4	82.7	20	2	AAV23613	Aav23613 Homo sapi
	35	12.4	82.7	20	6	ABI94231	Abi94231 Capture o
	36	12.4	82.7	24	6	ABI85032	Abi85032 Capture o
c	37	12.4	82.7	24	6	ABI85033	Abi85033 Capture o
	38	12.4	82.7	27	2	AAV93971	Aav93971 Human IL-
	39	12	80.0	20	2	AAT27483	Aat27483 Human c-r
c	40	12	80.0	20	2	AAT86617	Aat86617 Rat c-raf
	41	12	80.0	20	2	AAZ11513	Aaz11513 Human c-r
	42	12	80.0	20	3	AAA92027	Aaa92027 C-raf tar
c	43	12	80.0	20	3	AAA92026	Aaa92026 C-raf tar
	44	12	80.0	20	3	AAA73491	Aaa73491 Human c-r
	45	12	80.0	20	6	AAD44716	Aad44716 Human c-r

ALIGNMENTS

RESULT 1
AAV54043
ID AAV54043 standard; DNA; 15 BP.
XX
AC AAV54043;
XX
DT 02-DEC-1998 (first entry)
XX
DE Human antisense c-raf-1 oligodeoxyribonucleotide.
XX
KW Human; antisense; c-raf-1; oligodeoxyribonucleotide; ODN/oligo;
KW tumour tissue; cancer; radiation therapy; radiosensitise; antisense;
KW liposome carrier system; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1
FT /*tag= a
FT /note= "N-terminal base is phosphothioated"
FT modified_base 15
FT /*tag= b
FT /note= "C-terminal base is phosphothioated"
XX
PN WO9843095-A1.
XX
PD 01-OCT-1998.
XX
PF 19-MAR-1998; 98WO-US005303.
XX
PR 21-MAR-1997; 97US-0041192P.
PR 24-OCT-1997; 97US-00957327.
XX
PA (GEOU) UNIV GEORGETOWN.
XX
PI Kasid U, Gokhale P, Dritschilo A, Rahman A;
XX
DR WPI; 1998-532155/45.
XX
PT New cationic liposome composition containing raf oligodeoxynucleotide -
PT can be used to directly target tumour tissue and is useful in the
PT radiation therapy of cancers.
XX

```
PS   Claim 4; Page 21; 25pp; English.
XX
CC   This is the nucleotide sequence of the human antisense c-raf-1
CC   oligodeoxyribonucleotide (ODN/oligo), used in the method of the invention
CC   to directly target tumour tissue, and in cancer radiation therapy. The
CC   products can be used in a method of radiosensitising tumour tissue by
CC   addition of an antisense oligonucleotide of maximum 40 bases containing
CC   ODN/oligo. The liposome carrier system directly targets tumour tissue and
CC   has the potential for use in the radiation therapy of cancers
XX
SQ   Sequence 15 BP; 2 A; 4 C; 4 G; 5 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 15;  DB 2;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATGC 15
              |||||||||||||||
Db          1 GTGCTCCATTGATGC 15


RESULT 2
AAV99435
ID   AAV99435 standard; DNA; 15 BP.
XX
AC   AAV99435;
XX
DT   22-MAR-1999  (first entry)
XX
DE   Antisense oligonucleotide directed against c-raf-1 protein kinase gene.
XX
KW   Antisense oligonucleotide; human c-raf-1 protein kinase gene;
KW   phosphorothioate; phosphodiester; lipid-encapsulation; tumour;
KW   aberrant gene expression; treatment; inflammation; infection; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .15
FT                    /*tag=  a
FT                    /note= "phosphorothioate or phosphodiester bonds"
XX
PN   WO9851278-A2.
XX
PD   19-NOV-1998.
XX
PF   14-MAY-1998;   98WO-CA000485.
XX
PR   14-MAY-1997;   97US-00856374.
XX
PA   (INEX-) INEX PHARM CORP.
XX
PI   Semple SC,  Klimuk SK,  Harasym T,  Hope MJ,  Ansell SM,  Cullis P;
PI   Scherrer P,  Debeyer D;
XX
DR   WPI; 1999-045179/04.
XX
PT   Composition containing lipid-encapsulated therapeutic agent - useful,
PT   e.g. for delivering antisense molecules or ribozymes or treating diseases
PT   associated with aberrant gene expression.
XX
PS   Disclosure; Page 23; 98pp; English.
XX
CC   The present sequence represents an antisense oligonucleotide directed
CC   against the human c-raf-1 protein kinase gene. The oligonucleotide can
CC   have either phosphorothioate or phosphodiester bonds. The oligonucleotide
CC   is lipid-encapsulated using the method of the invention. A composition
CC   comprising lipid-encapsulated particles of a therapeutic agent, e.g.
CC   antisense oligonucleotides, is prepared by mixing at least 2 lipids with
CC   buffered aqueous solution of charged therapeutic agent to form an
CC   intermediate mixture of lipid-encapsulated particles, and changing the pH
CC   of the mixture to neutralise at least some of the external surface
CC   charges on the particles. One lipid has a (de)protonatable group with Ka
CC   such that the lipid is charged at a first pH but neutral at a second pH
CC   (particularly near physiological pH) and the buffer maintains this lipid
CC   in the charged form (i.e. cationic when the therapeutic agent is anionic
CC   in the buffer, or vice versa). The second lipid prevents particle
CC   aggregation during formation of the lipid-therapeutic agent particles.
CC   The composition is used to introduce therapeutic agents into cells, in
CC   vivo or in vitro, particularly to treat or prevent diseases associated
CC   with aberrant gene expression in mammals, specifically tumours,
CC   inflammation or infection
XX
SQ   Sequence 15 BP; 2 A; 4 C; 4 G; 5 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 15;  DB 2;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATGC 15
              |||||||||||||||
Db          1 GTGCTCCATTGATGC 15


RESULT 3
AAZ98661
ID   AAZ98661 standard; DNA; 15 BP.
XX
AC   AAZ98661;
XX
DT   05-JUN-2000  (first entry)
XX
DE   Human c-raf-1 PK therapeutic antisense oligonucleotide sequence ATG-AS.
XX
KW   Antisense oligonucleotide; phosphorothioate; inflammatory disease;
KW   tumour; gene therapy; aberrant gene expression; treatment;
KW   infectious disease; protein kinase C alpha; c-raf-1 protein kinase; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   misc_feature     1. .15
FT                    /*tag=  a
FT                    /note= "Optionally phosphorothioate internucleotide
FT                    linkages"
XX
PN   CA2271582-A1.
XX
PD   14-NOV-1999.
XX
PF   13-MAY-1999;   99CA-02271582.
XX
PR   14-MAY-1998;   98US-00078955.
XX
PA   (KLIM/) KLIMUK S K.
PA   (HARA/) HARASYM T.
PA   (HOPE/) HOPE M J.
PA   (ANSE/) ANSELL S M.
PA   (CULL/) CULLIS P R.
PA   (MOKW/) MOK W W K.
PA   (SCHE/) SCHERRER P.
PA   (SEMP/) SEMPLE S C.
XX
PI   Klimuk SK,  Harasym T,  Hope MJ,  Ansell SM,  Cullis PR,  Mok WWK;
PI   Scherrer P,  Semple SC;
XX
DR   WPI; 2000-225058/20.
XX
PT   A method for delivering antisense oligonucleotides to cells using lipid
PT   capsules comprising steric barrier lipids.
XX
PS   Example 5; Page 57; 99pp; English.
XX
CC   This sequence represents an antisense oligonucleotide sequence which has
CC   human c-raf-1 protein kinase as its target gene. The oligonucleotide is
```

```
CC   used in a method for delivering lipid encapsulated therapeutic agents
CC   (i.e antisense oligonucleotides) to mammals. The lipid capsule comprises
CC   steric barrier lipids that prevent particle aggregation during lipid
CC   nucleic acid formation. The method may be used for the delivery of
CC   therapeutic agents to mammalian cells. It is especially suitable for
CC   delivering nucleic acid molecules, and in particular antisense molecules
CC   which may be administered to down regulate the expression of aberrant
CC   genes. The aberrant gene may be ICAM-1, c-myc, c-myb, ras, raf, erb-B-2,
CC   PKC-alpha, IGF-1R, EGFR, VEGF and/or VEG-R-1. The method may be used for
CC   the treatment of tumours, inflammatory diseases and/or infectious
CC   diseases
XX
SQ   Sequence 15 BP; 2 A; 4 C; 4 G; 5 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 15;  DB 3;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATGC 15
              |||||||||||||||
Db          1 GTGCTCCATTGATGC 15


RESULT 4
AAD22797
ID   AAD22797 standard; DNA; 15 BP.
XX
AC   AAD22797;
XX
DT   26-FEB-2002  (first entry)
XX
DE   Human c-raf-1 protein kinase antisense oligonucleotide, ATG-AS.
XX
KW   Treatment; tumour; lipid-therapeutic agent particle; sphingomyelin;
KW   distearoylphosphatidylcholine; palmitoyloleoyl phophatidylcholine; DSPC;
KW   POPC; 1,2-dioleoyl-sn-3-phosphoethanolamine; cholesterol; SM; DOPE;
KW   inflammation; c-raf-1 protein kinase gene; human; infectious disease; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "Optionally phosphorothioate backbone"
XX
PN   US6287591-B1.
XX
PD   11-SEP-2001.
XX
PF   14-MAY-1998;   98US-00078954.
XX
PR   14-MAY-1997;   97US-00856374.
XX
PA   (INEX-) INEX PHARM CORP.
XX
PI   Semple SC,  Klimuk SK,  Harasym T,  Hope MJ,  Ansell SM,  Cullis P;
PI   Scherrer P,  Debeyer D;
XX
DR   WPI; 2002-024658/03.
XX
PT   Composition useful for treatment of e.g. tumors comprises particles
PT   comprising lipid portion and a charged therapeutic agent.
XX
PS   Disclosure; Col 15-16; 48pp; English.
XX
CC   The invention relates to a composition useful for treatment of e.g.
CC   tumours. The composition comprises lipid-therapeutic agent particles
CC   comprising a lipid portion and a charged therapeutic agent which is
CC   encapsulated in the lipid portion. The lipid portion comprises a first
CC   lipid component selected from lipids containing a protonatable or
CC   deprotonatable (preferably protonatable) group that has a pKa such that
CC   the lipid is in charged form at a first pH and in neutral form at a
CC   second pH. The pKa of lipid component is from 4-11. The first lipid
CC   component is further selected such that the charged form is cationic when
CC   the therapeutic agent is anionic and vice versa; the second lipid
CC   component is selected from lipids that prevent particle aggregation
CC   during lipid-therapeutic agent particles formation and which exchange out
CC   the lipid particle at a rate greater than PEG-CerC20; third lipid
CC   component is a neutral lipid selected from distearoylphosphatidylcholine
CC   (DSPC), palmitoyloleoyl phophatidylcholine (POPC), 1,2-dioleoyl-sn-3-
CC   phosphoethanolamine (DOPE) or SM (sphingomyelin) and a fourth lipid
CC   component which is cholesterol. Compositions of the invention are used
CC   for treatment or prevention of a disease caused by aberrant expression of
CC   a gene preferably ICAM-1 (Intracellular adhesion molecule-1), c-myc, c-
CC   myb, ras, raf, erb-B-2, PKC-alpha (phosphokinase C-alpha), IGF-1R
CC   (insulin growth factor 1-receptor), bcl-2, EGFR (epidermal growth factor
CC   receptor), VEGF and VEGF-R-1 (vascular endothelial growth factor receptor
CC   1) in a mammal or by inflammations such as tumour or an infectious
CC   disease. The present sequence is an antisense oligonucleotide targetted
CC   to human c-raf-1 protein kinase gene
XX
SQ   Sequence 15 BP; 2 A; 4 C; 4 G; 5 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 15;  DB 6;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATGC 15
              |||||||||||||||
Db          1 GTGCTCCATTGATGC 15


RESULT 5
ACC58517
ID   ACC58517 standard; DNA; 15 BP.
XX
AC   ACC58517;
XX
DT   26-AUG-2003  (first entry)
XX
DE   Oligonucleotide ODN #25 (hC-Raf1).
XX
KW   Lipid nucleic acid; LNA; mucosal; vaccine; immunostimulant; human;
KW   C-Raf-s; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .15
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "OTHER= optional phosphorothioate nucleotides"
XX
PN   WO2003039595-A2.
XX
PD   15-MAY-2003.
XX
PF   07-NOV-2002; 2002WO-CA001717.
XX
PR   07-NOV-2001; 2001US-0337522P.
PR   10-MAY-2002; 2002US-0379343P.
XX
PA   (INEX-) INEX PHARM CORP.
XX
PI   Semple S,  Klimuk S,  Yuan Z;
XX
DR   WPI; 2003-493235/46.
XX
PT   Improved mucosal adjuvant useful in the preparation of vaccine for
PT   stimulating an immune response comprises a lipid-nucleic acid formulation
PT   containing a nucleic acid component encapsulated by a lipid.
XX
PS   Disclosure; Page 21; 71pp; English.
XX
CC   The present sequence is that of oligodeoxynucleotide ODN #25 (hC-Raf-1)
```

```
CC   for human C-Raf-s. It is an example of an ODN that can be used in lipid-
CC   nucleic acid (LNA) formulations of the invention comprising a lipid
CC   component and a nucleic acid component. The invention is based on the
CC   discovery that such LNA formulations associated with a target antigen
CC   stimulate enhanced mucosal immune responses, especially IgA production,
CC   directed to that target antigen in vivo as compared to the target antigen
CC   alone or mixed with free or unencapsulated forms of the ODN. Claimed
CC   improved mucosal vaccines comprise an LNA formulation with at least one
CC   antigen, the LNA formulation comprising a lipid component that
CC   encapsulates the nucleic acid component, with the lipid and nucleic acid
CC   components acting synergistically to stimulate antigen-specific IgG
CC   production in a mammal
XX
SQ   Sequence 15 BP; 2 A; 4 C; 4 G; 5 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 15;  DB 9;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATGC 15
              |||||||||||||||
Db          1 GTGCTCCATTGATGC 15


RESULT 6
ADA24233
ID   ADA24233 standard; DNA; 15 BP.
XX
AC   ADA24233;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human c-raf-1 protein kinase antisense oligonucleotide SEQ ID NO:16.
XX
KW   therapeutic oligonucleotide; double-stranded RNA; dsRNA; mobile protein;
KW   cytostatic; immunosuppressive; virucide; anti-HIV; antibacterial;
KW   cardiant; hyperproliferation; cancer; haematological; metastatic;
KW   autoimmune disease; infection; endocrine; neural; cardiovascular;
KW   pulmonary; reproductive system disorder; endocytosis; metabolic process;
KW   murine; intracellular adhesion molecule 1; ICAM-1;
KW   antisense oligonucleotide; phosphorothioate; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .15
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "optionally phosphorothioate backbone"
XX
PN   WO2003069306-A2.
XX
PD   21-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004323.
XX
PR   13-FEB-2002; 2002US-0356053P.
XX
PA   (MEDB-) MEDBRIDGE INC.
XX
PI   Xie D;
XX
DR   WPI; 2003-646491/61.
XX
PT   Treating diseases with oligonucleotides or interfering RNA, useful e.g.
PT   for cancer or autoimmune diseases, covalently coupled to mobile proteins,
PT   in vivo or in vitro.
XX
PS   Claim 128; Page 12; 42pp; English.
XX
CC   The present invention describes a method for treating a disease by
CC   administering: (a) a therapeutic oligonucleotide (TON) or double-stranded
CC   RNA (dsRNA) that includes a reactive group (RG) that can react with a
CC   mobile protein (MP) to form a covalent conjugate of TON/dsRNA and MP; or
CC   (b) TON or dsRNA already conjugated to MP through a covalent bond. Also
CC   described: (1) TON of 15-30 bases that includes (i) a part that binds to
CC   target RNA or DNA and (ii) RG; (2) TON of 15-30 bases that includes a
CC   part that binds to target RNA or DNA and is conjugated to MP through a
CC   covalent link; (3) dsRNA that includes RG; and (4) dsRNA that is
CC   conjugated to MP through a covalent link. TON have cytostatic,
CC   immunosuppressive, virucide, anti-HIV, antibacterial and cardiant
CC   activities. The method is used to treat, or prevent, hyperproliferation
CC   (particularly cancers, solid or haematological, including prevention of
CC   metastatic spread); autoimmune diseases; viral or bacterial infections;
CC   endocrine, neural, cardiovascular, pulmonary or reproductive system
CC   disorders. Also where TON or dsRNA are labelled, they can be used for
CC   diagnosis and monitoring of therapy. When linked to a mobile protein,
CC   TON/dsRNA have better cell entry (via endocytosis or other parts of the
CC   mobile protein metabolic process) and longer therapeutic life, increased
CC   from hours to weeks (the result of increased resistance to nuclease),
CC   without loss of affinity for the target. In many cases immune response to
CC   TON/dsRNA is also reduced, as is non-specific binding to endogenous
CC   proteins. The present sequence represents a human c-raf-1 antisense
CC   oligonucleotide, which is a specifically claimed TON from the present
CC   invention.
XX
SQ   Sequence 15 BP; 2 A; 4 C; 4 G; 5 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 15;  DB 9;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATGC 15
              |||||||||||||||
Db          1 GTGCTCCATTGATGC 15


RESULT 7
ADB97458/c
ID   ADB97458 standard; DNA; 15 BP.
XX
AC   ADB97458;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Sense (ATG-S) raf ODN oligodeoxyribonucleotide.
XX
KW   antisense; ATG-S; raf ODN; chemosensitisation; tumour tissue;
KW   chemotherapeutic agent; cationic liposome; cationic lipid;
KW   phosphatidylcholine; cholesterol; liposome;
KW   dimethyldioctadecyl ammonium bromide; DDAB;
KW   dimyristoyl trimethyl ammonium propane; DMTAP; phosphatidylcholine; PC;
KW   cholesterol; cancer; leukaemia; lymphoma; myeloma; carcinoma; sarcoma;
KW   combination therapy; pre-cancerous lesion; chemotherapy; ss.
XX
OS   Unidentified.
XX
PN   WO2003070221-A1.
XX
PD   28-AUG-2003.
XX
PF   14-FEB-2003; 2003WO-US004681.
XX
PR   15-FEB-2002; 2002US-00075994.
XX
PA   (GEOU ) UNIV GEORGETOWN.
PA   (NEOP-) NEOPHARM INC.
XX
PI   Kasid U,  Gokhale P,  Pei J,  Mewani R,  Ahmad I,  Drischilo A;
PI   Rahman A;
XX
DR   WPI; 2003-689738/65.
XX
PT   Chemosensitization of tumor tissue, useful for treating cancer, e.g.
PT   leukemia, lymphoma or myeloma, comprises administering a chemotherapeutic
```

PT agent and cationic liposomes containing oligonucleotides.
XX
PS Example 1; Page 18; 77pp; English.
XX
CC The invention relates to a novel method for the chemosensitisation of
CC tumour tissue, comprising administering a chemotherapeutic agent and a
CC composition comprising cationic liposomes consisting of cationic lipid,
CC phosphatidylcholine and cholesterol, where oligonucleotide(s) are
CC encapsulated within the liposome. The invention further relates to a
CC composition comprising liposomes consisting essentially of a cationic
CC lipid like dimethyldioctadecyl ammonium bromide (DDAB) or dimyristoyl
CC trimethyl ammonium propane (DMTAP), phosphatidylcholine (PC),
CC cholesterol, and containing the sequence 5'- GTGCTCCATTGATGC -3', where
CC only the terminal sequences are phosphorothioated. The method is useful
CC for chemosensitisation of a tumour tissue or cancer, including leukaemia,
CC lymphoma, myeloma, carcinoma or sarcoma. The combination therapy may be
CC used for any stage of cancer ranging from pre-cancerous lesions to cancer
CC of advanced stages. This polynucleotide sequence represents the sense
CC (ATG-S) raf ODN oligodeoxyribonucleotide, a cationic liposome of the
CC invention.
XX
SQ Sequence 15 BP; 5 A; 4 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 15; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCTCCATTGATGC 15
||||||||||||||||
Db 15 GTGCTCCATTGATGC 1

RESULT 8
ADB97456
ID ADB97456 standard; DNA; 15 BP.
XX
AC ADB97456;
XX
DT 04-DEC-2003 (first entry)
XX
DE Antisense (ATG-AS) raf ODN oligodeoxyribonucleotide.
XX
KW antisense; ATG-AS; raf ODN; chemosensitisation; tumour tissue;
KW chemotherapeutic agent; cationic liposome; cationic lipid;
KW phosphatidylcholine; cholesterol; liposome;
KW dimethyldioctadecyl ammonium bromide; DDAB;
KW dimyristoyl trimethyl ammonium propane; DMTAP; phosphatidylcholine; PC;
KW cholesterol; cancer; leukaemia; lymphoma; myeloma; carcinoma; sarcoma;
KW combination therapy; pre-cancerous lesion; chemotherapy; ss.
XX
OS Unidentified.
XX
PN WO2003070221-A1.
XX
PD 28-AUG-2003.
XX
PF 14-FEB-2003; 2003WO-US004681.
XX
PR 15-FEB-2002; 2002US-00075994.
XX
PA (GEOU) UNIV GEORGETOWN.
PA (NEOP-) NEOPHARM INC.
XX
PI Kasid U, Gokhale P, Pei J, Mewani R, Ahmad I, Drischilo A;
PI Rahman A;
XX
DR WPI; 2003-689738/65.
XX
PT Chemosensitization of tumor tissue, useful for treating cancer, e.g.
PT leukemia, lymphoma or myeloma, comprises administering a chemotherapeutic
PT agent and cationic liposomes containing oligonucleotides.
XX
PS Example 1; Page 18; 77pp; English.
XX
CC The invention relates to a novel method for the chemosensitisation of
CC tumour tissue, comprising administering a chemotherapeutic agent and a
CC composition comprising cationic liposomes consisting of cationic lipid,
CC phosphatidylcholine and cholesterol, where oligonucleotide(s) are
CC encapsulated within the liposome. The invention further relates to a
CC composition comprising liposomes consisting essentially of a cationic
CC lipid like dimethyldioctadecyl ammonium bromide (DDAB) or dimyristoyl
CC trimethyl ammonium propane (DMTAP), phosphatidylcholine (PC),
CC cholesterol, and containing the sequence 5'- GTGCTCCATTGATGC -3', where
CC only the terminal sequences are phosphorothioated. The method is useful
CC for chemosensitisation of a tumour tissue or cancer, including leukaemia,
CC lymphoma, myeloma, carcinoma or sarcoma. The combination therapy may be
CC used for any stage of cancer ranging from pre-cancerous lesions to cancer
CC of advanced stages. This polynucleotide sequence represents the antisense
CC (ATG-AS) raf ODN oligodeoxyribonucleotide, a cationic liposome of the
CC invention.
XX
SQ Sequence 15 BP; 2 A; 4 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 15; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCTCCATTGATGC 15
||||||||||||||||
Db 1 GTGCTCCATTGATGC 15

RESULT 9
ADF82830
ID ADF82830 standard; DNA; 15 BP.
XX
AC ADF82830;
XX
DT 26-FEB-2004 (first entry)
XX
DE Immunostimulant ODN25, component of lipid-nucleic acid vaccine.
XX
KW Immunostimulant; vaccine; lipid-nucleic acid; phosphorothioate; human;
KW C-Raf-s; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1. .15
FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER= optional phosphorothioate nucleotides"
XX
PN WO2003094829-A2.
XX
PD 20-NOV-2003.
XX
PF 12-MAY-2003; 2003WO-CA000680.
XX
PR 10-MAY-2002; 2002US-0379343P.
PR 07-NOV-2002; 2002US-00290545.
PR 12-MAR-2003; 2003US-0454298P.
XX
PA (INEX-) INEX PHARM CORP.
XX
PI Semple S, Chikh G, Hope MJ, Tam YK;
XX
DR WPI; 2003-903935/82.
XX
PT New pathogen vaccine having a lipid-nucleic acid formulation in
PT combination with at least one microbial antigen, useful for stimulating
PT enhanced responses against bacterial, viral and parasitic infections.
XX
PS Disclosure; SEQ ID NO 25; 138pp; English.
XX

```
CC   The present sequence is that of ODN25 (C-Raf-s) for human C-Raf-s. This
CC   is an immunostimulatory oligonucleotide that can be used in lipid-nucleic
CC   acid (LNA) vaccines of the invention. Claimed vaccines comprise an LNA
CC   formulation in combination with at least one microbial antigen, such as
CC   hepatitis B virus surface antigen. The lipid component of the LNA
CC   comprises at least one cationic lipid. The oligonucleotide component of
CC   the LNA preferably comprises at least one CpG dinucleotide, a methylated
CC   cytosine and a phosphorothioate backbone. The vaccine is capable of
CC   stimulating Th1 type humoral and cellular immune responses. An enhanced
CC   humoral response is demonstrated by a strong early peak of interferon-
CC   gamma production observed within hours of vaccine followed by a second
CC   stronger peak of interferon-gamma production observed several days later,
CC   correlated with antibody isotype switching.
XX
SQ   Sequence 15 BP; 2 A; 4 C; 4 G; 5 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 15;  DB 10;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATGC 15
              |||||||||||||||
Db          1 GTGCTCCATTGATGC 15


RESULT 10
ADE90171
ID   ADE90171 standard; DNA; 15 BP.
XX
AC   ADE90171;
XX
DT   12-FEB-2004  (first entry)
XX
DE   Human c-raf-1 protein kinase antisense oligonucleotide.
XX
KW   ss; lipid-encapsulated therapeutic agent particle;
KW   aberrant gene expression; intercellular adhesion molecule; ICAM-1; c-myc;
KW   c-myb; ras; raf; erb-B-2; protein kinase C; PKC-alpha;
KW   insulin-like growth factor; IGF-IR; epidermal growth factor receptor;
KW   EGFR; vascular endothelial growth factor; VEGF; VEGF-R-1; tumour;
KW   inflammation; infection; antisense; human.
XX
OS   Homo sapiens.
XX
PN   US2003129221-A1.
XX
PD   10-JUL-2003.
XX
PF   29-JUN-2001; 2001US-00895480.
XX
PR   14-MAY-1997;   97US-00856374.
PR   14-MAY-1998;   98US-00078954.
XX
PA   (SEMP/) SEMPLE S C.
PA   (KLIM/) KLIMUK S K.
PA   (HARA/) HARASYM T.
PA   (HOPE/) HOPE M J.
PA   (ANSE/) ANSELL S M.
PA   (CULL/) CULLIS P.
PA   (SCHE/) SCHERRER P.
PA   (DEBE/) DEBEYER D.
XX
PI   Semple SC,  Klimuk SK,  Harasym T,  Hope MJ,  Ansell SM,  Cullis P;
PI   Scherrer P,  Debeyer D;
XX
DR   WPI; 2004-031296/03.
XX
PT   Preparation of a composition comprising lipid-encapsulated therapeutic
PT   agent particles, useful for introducing a nucleic acid into a cell and
PT   for treating diseases characterized by aberrant gene expression.
XX
PS   Disclosure; SEQ ID NO 15; 52pp; English.
XX
CC   The invention relates to a method of preparation of a composition
CC   comprising lipid-encapsulated therapeutic agent particles. The
CC   composition is useful for introducing a nucleic acid into a cell and for
CC   treating diseases characterized by aberrant gene expression (especially
CC   intercellular adhesion molecule (ICAM)-1, c-myc, c-myb, ras, raf erb-B-2,
CC   protein kinase C (PKC)-alpha, insulin-like growth factor (IGF)-IR,
CC   epidermal growth factor receptor (EGFR), vascular endothelial growth
CC   factor (VEGF) or VEGF-R-1), e.g. tumours, inflammation or infection. The
CC   present sequence represents an antisense oligonucletide.
XX
SQ   Sequence 15 BP; 2 A; 4 C; 4 G; 5 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 15;  DB 12;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATGC 15
              |||||||||||||||
Db          1 GTGCTCCATTGATGC 15


RESULT 11
ADE39690
ID   ADE39690 standard; DNA; 15 BP.
XX
AC   ADE39690;
XX
DT   12-FEB-2004  (first entry)
XX
DE   Oligonucleotide ODN 25 (hC-Raf-1) SEQ ID NO:25.
XX
KW   cancer; vaccine; lipid-nucleic acid; LNA; tumour-associated antigen;
KW   Th-1 based immune response; cytostatic; gene therapy;
KW   tumour growth inhibition; tumour; human; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .15
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "optionally phosphorothioate linkages"
XX
PN   WO2003094828-A2.
XX
PD   20-NOV-2003.
XX
PF   12-MAY-2003; 2003WO-CA000679.
XX
PR   10-MAY-2002; 2002US-0379343P.
PR   07-NOV-2002; 2002US-00290545.
PR   04-APR-2003; 2003US-0460646P.
XX
PA   (INEX-) INEX PHARM CORP.
XX
PI   Tam YK,  Semple S,  Klimuk S,  Chikh G;
XX
DR   WPI; 2004-011992/01.
XX
PT   New cancer vaccine having a lipid-nucleic acid formulation in combination
PT   with at least one tumor-associated antigen, useful for stimulating
PT   enhanced responses against tumor-associated antigens and for inhibiting
PT   tumor growth.
XX
PS   Example 9; SEQ ID NO 25; 119pp; English.
XX
CC   The present invention describes a cancer vaccine (I), which comprises a
CC   lipid-nucleic acid (LNA) formulation in combination with at least one
CC   tumour-associated antigen that is mixed with or associated with the LNA
CC   formulation comprising a lipid component having at least one cationic
CC   lipid, and a nucleic acid component comprising at least one
CC   oligonucleotide, where the vaccine is capable of stimulating a Th-1 based
```

```
CC   immune response in vivo to the at least one tumour-associated antigen.
CC   (I) has cytostatic activity, and can be used in vaccines, and in gene
CC   therapy. The methods and compositions of the present invention can be
CC   used for stimulating enhanced responses against tumour-associated
CC   antigens and for inhibiting tumour growth. The present sequence
CC   represents an oligonucleotide which is used in the exemplification of the
CC   present invention.
XX
SQ   Sequence 15 BP; 2 A; 4 C; 4 G; 5 T; 0 U; 0 Other;

  Query Match            100.0%;  Score 15;  DB 12;  Length 15;
  Best Local Similarity  100.0%;  Pred. No. 1.1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATGC 15
              |||||||||||||||
Db          1 GTGCTCCATTGATGC 15


RESULT 12
ADF32025
ID   ADF32025 standard; DNA; 15 BP.
XX
AC   ADF32025;
XX
DT   26-FEB-2004  (first entry)
XX
DE   Antisense oligonucleotide of the invention.
XX
KW   platelet; oligonucleotide; Thrombolytic; thrombocytosis; ss.
XX
OS   Synthetic.
XX
PN   WO2003099213-A2.
XX
PD   04-DEC-2003.
XX
PF   19-MAY-2003; 2003WO-US015922.
XX
PR   20-MAY-2002; 2002US-0382411P.
XX
PA   (NEOP-) NEOPHARM INC.
XX
PI   Gately ST;
XX
DR   WPI; 2004-035033/03.
XX
PT   Reducing the platelet count in a patient, useful for treating
PT   thrombocytosis, comprises administering antisense oligonucleotides
PT   inhibiting raf-1 gene with an agent that enhances penetration of the
PT   oligonucleotide into cells.
XX
PS   Example 1; SEQ ID NO 1; 14pp; English.
XX
CC   The present invention relates to reducing the platelet count in a patient
CC   comprises preparing a formulation of an oligonucleotide with an agent
CC   that enhances penetration of the oligonucleotide into cells, and
CC   administering the formulation to a patient having an elevated platelet
CC   count. The oligonucleotide is useful for preparing a medicament for
CC   reducing the platelet count in a patient, particularly for treating
CC   thrombocytosis. The present sequence represents an oligonucleotide of the
CC   invention.
XX
SQ   Sequence 15 BP; 2 A; 4 C; 4 G; 5 T; 0 U; 0 Other;

  Query Match            100.0%;  Score 15;  DB 12;  Length 15;
  Best Local Similarity  100.0%;  Pred. No. 1.1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATGC 15
              |||||||||||||||
Db          1 GTGCTCCATTGATGC 15


RESULT 13
ADF42926
ID   ADF42926 standard; DNA; 15 BP.
XX
AC   ADF42926;
XX
DT   11-MAR-2004  (first entry)
XX
DE   Methylated immunostimulatory oligonucleotide ODN 25 SEQ ID NO:25.
XX
KW   lipid-methylated nucleic acid formulation; immune response;
KW   lipid-nucleic acid; vaccine; immunostimulant; cytostatic;
KW   antiinflammatory; antiarthritic; gene therapy; cancer; inflammation;
KW   arthritis; immunodeficiency disorder;
KW   methylated immunostimulatory oligonucleotide; ss.
XX
OS   Synthetic.
XX
PN   WO2003094963-A2.
XX
PD   20-NOV-2003.
XX
PF   12-MAY-2003; 2003WO-CA000678.
XX
PR   10-MAY-2002; 2002US-0379343P.
PR   07-NOV-2002; 2002US-00290545.
PR   04-APR-2003; 2003US-0460646P.
XX
PA   (INEX-) INEX PHARM CORP.
XX
PI   Tam YK,  Semple S,  Klimuk S,  Chikh G;
XX
DR   WPI; 2004-142698/14.
XX
PT   Lipid-methylated nucleic acid formulation for stimulating an immune
PT   response in an animal comprises a lipid component and a nucleic acid
PT   component comprising a methylated nucleic acid sequence.
XX
PS   Disclosure; SEQ ID NO 25; 102pp; English.
XX
CC   The present invention describes a lipid-methylated nucleic acid
CC   formulation for stimulating an immune response in an animal, comprising a
CC   lipid component and a nucleic acid component which is a methylated
CC   nucleic acid sequence. Also described: (1) an adjuvant comprising a lipid
CC   -nucleic acid (LNA) formulation; (2) a vaccine comprising the LNA
CC   formulation in combination with at least one target antigen; (3)
CC   stimulating an enhanced host immune response to antigenic stimulation,
CC   comprising administering to the host the LNA formulation; (4) stimulating
CC   host dendritic cells in vivo, comprising contacting at least one
CC   dendritic cell with the lipid-methylated nucleic acid formulation to a
CC   host; and (5) simultaneously delivering antigenic and adjuvant immune
CC   stimulation to antigen presenting cells, comprising the administration of
CC   the LNA formulation associated with a target antigen. The lipid-
CC   methylation nucleic acid formulation has immunostimulant, cytostatic,
CC   antiinflammatory and antiarthritic activities, and can be used in
CC   vaccines, and in gene therapy. The formulation and methods are useful in
CC   stimulating a host's immune response to antigenic stimulation, or in
CC   activating and/or expanding dendritic cell populations in response to
CC   antigenic stimulation. They may be used for treating cancer,
CC   inflammation, arthritis or immunodeficiency disorders. The present
CC   sequence represents a methylated immunostimulatory oligonucleotide given
CC   in the exemplification of the present invention.
XX
SQ   Sequence 15 BP; 2 A; 4 C; 4 G; 5 T; 0 U; 0 Other;

  Query Match            100.0%;  Score 15;  DB 12;  Length 15;
  Best Local Similarity  100.0%;  Pred. No. 1.1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATGC 15
              |||||||||||||||
Db          1 GTGCTCCATTGATGC 15
```

RESULT 14
ADL70154
ID ADL70154 standard; DNA; 15 BP.
XX
AC ADL70154;
XX
DT 20-MAY-2004 (first entry)
XX
DE Oligonucleotide antisense to raf.
XX
KW Raf; antisense; liposome; drug delivery; cytostatic; ss.
XX
OS Synthetic.
XX
PN WO2004017944-A1.
XX
PD 04-MAR-2004.
XX
PF 13-AUG-2003; 2003WO-US025293.
XX
PR 23-AUG-2002; 2002US-0405378P.
XX
PA (NEOP-) NEOPHARM INC.
XX
PI Zhang J, Ahmad I;
XX
DR WPI; 2004-257219/24.
XX
PT Treatment of cellular proliferative disease e.g. cancer involves
PT administration of a composition comprising liposomal gemcitabine and
PT negatively charged phospholipid.
XX
PS Disclosure; SEQ ID NO 1; 25pp; English.
XX
CC The present sequence is that of an antisense oligonucleotide to raf. The
CC invention relates to novel gemcitabine compositions and their use in
CC treating proliferative diseases such as cancer, particularly in mammals,
CC especially in humans. The compositions include liposome-entrapped
CC gemcitabine. The cancer is especially lymphoma, ovarian cancer, breast
CC cancer, pancreatic cancer, lung cancer or colon cancer. The liposomal
CC gemcitabine compositions can be used in conjunction with secondary
CC therapeutic agents including antineoplastic, antifungal and antibiotic
CC agents as well as antisense oligonucleotides, especially an antisense
CC oligonucleotide to raf (claimed).
XX
SQ Sequence 15 BP; 2 A; 4 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 15; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCTCCATTGATGC 15
||||||||||||||||
Db 1 GTGCTCCATTGATGC 15

RESULT 15
ADR88950
ID ADR88950 standard; DNA; 15 BP.
XX
AC ADR88950;
XX
DT 18-NOV-2004 (first entry)
XX
DE Anti c-raf-1 oligonucleotide.
XX
KW C-raf-1; liposomal; antineoplastic; cytostatic; cancer; antisense; ss.
XX
OS Synthetic.
XX
PN WO2004071466-A2.
XX
PD 26-AUG-2004.
XX
PF 11-FEB-2004; 2004WO-US004555.
XX
PR 11-FEB-2003; 2003US-0446895P.
XX
PA (NEOP-) NEOPHARM INC.
XX
PI Bhamidipati S, Ahmad Z, Ahmad I;
XX
DR WPI; 2004-635030/61.
XX
PT Preparation of liposomal composition used for treating e.g. cancer
PT involves dissolving lipid fraction in water miscible organic solvent and
PT mixing solvent solution with aqueous solution.
XX
PS Disclosure; Page 6; 27pp; English.
XX
CC The invention relates to the preparation of a liposomal composition. The
CC method involves: dissolving a lipid fraction in a water-miscible organic
CC solvent; and mixing the water-miscible organic solvent solution
CC comprising the lipid fraction with an aqueous solution under conditions
CC to form a bulk liposomal composition. The method further involves adding
CC at least one active principal to the water-miscible organic solvent prior
CC to the addition of the lipid fraction, or to the aqueous solution prior,
CC during or after the step (b), size-reducing the bulk liposomal
CC composition to obtain a size-reduced liposomal composition, freeing the
CC liposomal composition of the water-miscible organic solvent by
CC diafiltration using a tangential flow filtration process and sterile
CC filtration, sterile-filtering the liposomal composition and freeze-drying
CC the liposomal preparation. Step (b) involves adding the water-miscible
CC organic solvent solution to the aqueous solution while mixing and mixing
CC of solution following addition of water-miscible solvent comprising the
CC lipid fraction to the aqueous solution while cooling. The active
CC principal comprises at least one antineoplastic or antifungal agent
CC (preferably taxane, camptothecin or their derivatives, especially
CC paclitaxel or docetaxel). The composition is used for the treatment of
CC disease e.g. cancer. The composition eliminates the disease or its
CC symptoms, need not completely eradicate the effects of the disease,
CC reduces the severity of a disease, infection or reduction in the rate by
CC which a disease progresses within a patient. The method permits the
CC production of liposomal formulation on a commercial scale. The present
CC sequence represents an antisense oligonucleotide specific for c-raf-1,
CC that can be used as an active principal.
XX
SQ Sequence 15 BP; 2 A; 4 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 15; DB 13; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCTCCATTGATGC 15
||||||||||||||||
Db 1 GTGCTCCATTGATGC 15

Search completed: June 21, 2005, 05:32:37
Job time : 431 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: June 21, 2005, 03:52:11 ; Search time 1686 Seconds
(without alignments)
431.096 Million cell updates/sec

Title: US-10-075-994A-1
Perfect score: 15
Sequence: 1 gtgctccattgatgc 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 1839042

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	15	100.0	15	6	AR110775	AR110775 Sequence
c	2	15	100.0	15	6	AR110777	AR110777 Sequence
	3	15	100.0	15	6	AR167449	AR167449 Sequence
	4	15	100.0	15	6	CQ789712	CQ789712 Sequence
	5	15	100.0	15	6	AR310685	AR310685 Sequence
c	6	15	100.0	15	6	AR310687	AR310687 Sequence
	7	15	100.0	15	6	AX797662	AX797662 Sequence
	8	15	100.0	15	6	AX957646	AX957646 Sequence
	9	15	100.0	15	6	AX957740	AX957740 Sequence
	10	15	100.0	15	6	AX958145	AX958145 Sequence
	11	15	100.0	15	6	BD106498	BD106498 High effi
	12	15	100.0	20	6	AR073978	AR073978 Sequence
	13	15	100.0	20	6	AR216002	AR216002 Sequence
	14	15	100.0	25	6	AR110776	AR110776 Sequence
	15	15	100.0	25	6	AR310686	AR310686 Sequence
c	16	14	93.3	35	10	AB112659S1	AB112659 Mus muscu
	17	13	86.7	20	6	AR073933	AR073933 Sequence
	18	13	86.7	20	6	AR105501	AR105501 Sequence
	19	13	86.7	20	6	E49512	E49512 Antisense o
	20	13	86.7	20	6	I27232	I27232 Sequence 2
	21	13	86.7	20	6	AR215955	AR215955 Sequence
c	22	12.4	82.7	20	6	AR037100	AR037100 Sequence
c	23	12.4	82.7	20	6	AR070338	AR070338 Sequence
	24	12.4	82.7	20	6	AX294189	AX294189 Sequence
	25	12.4	82.7	21	6	AX598466	AX598466 Sequence
	26	12.4	82.7	24	6	AX289556	AX289556 Sequence
	27	12.4	82.7	27	6	AR039324	AR039324 Sequence
c	28	12.4	82.7	43	6	CQ749113	CQ749113 Sequence
	29	12	80.0	20	6	AR073934	AR073934 Sequence
c	30	12	80.0	20	6	AR106990	AR106990 Sequence
	31	12	80.0	20	6	AR106991	AR106991 Sequence
	32	12	80.0	20	6	E49513	E49513 Antisense o
	33	12	80.0	20	6	I27233	I27233 Sequence 3
	34	12	80.0	20	6	AR215956	AR215956 Sequence
	35	12	80.0	22	6	AR493387	AR493387 Sequence
	36	11.8	78.7	26	6	A16281	A16281 Oligonucleo
c	37	11.8	78.7	27	6	A16266	A16266 Oligonucleo
	38	11.8	78.7	27	6	A16267	A16267 Oligonucleo
c	39	11.8	78.7	27	6	AR080410	AR080410 Sequence
c	40	11.8	78.7	27	6	AR092534	AR092534 Sequence
c	41	11.8	78.7	27	6	AR122889	AR122889 Sequence
c	42	11.8	78.7	27	6	AR123544	AR123544 Sequence
c	43	11.8	78.7	27	6	AR148361	AR148361 Sequence
	44	11.8	78.7	30	6	AR069912	AR069912 Sequence
c	45	11.8	78.7	33	6	BD014421	BD014421 Method fo

ALIGNMENTS

RESULT 1
AR110775
LOCUS AR110775 15 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 1 from patent US 6126965.
ACCESSION AR110775
VERSION AR110775.1 GI:12827623
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Kasid,U., Gokhale,P., Dritschilo,A. and Rahman,A.
TITLE Liposomes containing oligonucleotides
JOURNAL Patent: US 6126965-A 1 03-OCT-2000;
FEATURES Location/Qualifiers
source 1. .15
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN

Query Match 100.0%; Score 15; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCTCCATTGATGC 15
||||||||||||||
Db 1 GTGCTCCATTGATGC 15

RESULT 2
AR110777/c
LOCUS AR110777 15 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 3 from patent US 6126965.
ACCESSION AR110777
VERSION AR110777.1 GI:12827625
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Kasid,U., Gokhale,P., Dritschilo,A. and Rahman,A.
TITLE Liposomes containing oligonucleotides

```
  JOURNAL   Patent: US 6126965-A 3 03-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             100.0%;  Score 15;  DB 6;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATGC 15
              |||||||||||||||
Db         15 GTGCTCCATTGATGC 1


RESULT 3
AR167449
LOCUS       AR167449                  15 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 15 from patent US 6287591.
ACCESSION   AR167449
VERSION     AR167449.1  GI:17903229
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Semple,S.C., Klimuk,S.K., Harasym,T., Hope,M.J., Ansell,S.M.,
            Cullis,P., Scherrer,P. and Debeyer,D.
  TITLE     Charged therapeutic agents encapsulated in lipid particles
            containing four lipid components
  JOURNAL   Patent: US 6287591-A 15 11-SEP-2001;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             100.0%;  Score 15;  DB 6;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATGC 15
              |||||||||||||||
Db          1 GTGCTCCATTGATGC 15


RESULT 4
CQ789712
LOCUS       CQ789712                  15 bp    DNA     linear   PAT 29-MAR-2004
DEFINITION  Sequence 1 from Patent WO2004017944.
ACCESSION   CQ789712
VERSION     CQ789712.1  GI:45823264
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Zhang,J.A. and Ahmad,I.
  TITLE     Liposomal gemcitabine compositions for better drug delivery
  JOURNAL   Patent: WO 2004017944-A 1 04-MAR-2004;
            Neopharm, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Anti-raf-oligonucleotides"
ORIGIN

  Query Match             100.0%;  Score 15;  DB 6;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATGC 15
              |||||||||||||||
Db          1 GTGCTCCATTGATGC 15


RESULT 5
AR310685
LOCUS       AR310685                  15 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 1 from patent US 6559129.
ACCESSION   AR310685
VERSION     AR310685.1  GI:31703829
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kasid,U., Gokhale,P., Zhang,C., Dritschilo,A. and Rahman,A.
  TITLE     Cationic liposomal delivery system and therapeutic use thereof
  JOURNAL   Patent: US 6559129-A 1 06-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             100.0%;  Score 15;  DB 6;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATGC 15
              |||||||||||||||
Db          1 GTGCTCCATTGATGC 15


RESULT 6
AR310687/c
LOCUS       AR310687                  15 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 3 from patent US 6559129.
ACCESSION   AR310687
VERSION     AR310687.1  GI:31703831
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kasid,U., Gokhale,P., Zhang,C., Dritschilo,A. and Rahman,A.
  TITLE     Cationic liposomal delivery system and therapeutic use thereof
  JOURNAL   Patent: US 6559129-A 3 06-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             100.0%;  Score 15;  DB 6;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATGC 15
              |||||||||||||||
Db         15 GTGCTCCATTGATGC 1


RESULT 7
AX797662
LOCUS       AX797662                  15 bp    DNA     linear   PAT 04-OCT-2003
DEFINITION  Sequence 25 from Patent WO03039595.
ACCESSION   AX797662
VERSION     AX797662.1  GI:37518090
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
```

```
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
  AUTHORS  Semple,S., Klimuk,S. and Yuan,Z.N.
  TITLE    Mucosal adjuvants comprising an oligonucleotide and a cationic
           lipid
  JOURNAL  Patent: WO 03039595-A 25 15-MAY-2003;
           Inex Pharmaceuticals Corp. (CA)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match           100.0%;  Score 15;  DB 6;  Length 15;
  Best Local Similarity  100.0%;  Pred. No. 1.2e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATGC 15
              |||||||||||||||
Db          1 GTGCTCCATTGATGC 15


RESULT 8
AX957646
LOCUS       AX957646                 15 bp    DNA     linear   PAT 08-JAN-2004
DEFINITION  Sequence 25 from Patent WO03094963.
ACCESSION   AX957646
VERSION     AX957646.1  GI:40785518
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Tam,Y.K., Semple,S., Klimuk,S. and Chikh,G.
  TITLE     Methylated immunostimulatory oligonucleotides and methods of using
            the same
  JOURNAL   Patent: WO 03094963-A 25 20-NOV-2003;
            Inex Pharmaceuticals Corporation (CA)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match           100.0%;  Score 15;  DB 6;  Length 15;
  Best Local Similarity  100.0%;  Pred. No. 1.2e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATGC 15
              |||||||||||||||
Db          1 GTGCTCCATTGATGC 15


RESULT 9
AX957740
LOCUS       AX957740                 15 bp    DNA     linear   PAT 08-JAN-2004
DEFINITION  Sequence 25 from Patent WO03094828.
ACCESSION   AX957740
VERSION     AX957740.1  GI:40785558
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Tam,Y.K., Semple,S., Klimuk,S. and Chikh,G.
  TITLE     Cancer vaccines and methods of using the same
  JOURNAL   Patent: WO 03094828-A 25 20-NOV-2003;
            Inex Pharmaceuticals Corp. (CA)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match           100.0%;  Score 15;  DB 6;  Length 15;
  Best Local Similarity  100.0%;  Pred. No. 1.2e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATGC 15
              |||||||||||||||
Db          1 GTGCTCCATTGATGC 15


RESULT 10
AX958145
LOCUS       AX958145                 15 bp    DNA     linear   PAT 08-JAN-2004
DEFINITION  Sequence 25 from Patent WO03094829.
ACCESSION   AX958145
VERSION     AX958145.1  GI:40785809
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Semple,S., Chikh,G., Hope,M.J. and Tam,Y.K.
  TITLE     Pathogen vaccines and methods for using the same
  JOURNAL   Patent: WO 03094829-A 25 20-NOV-2003;
            Inex Pharmaceuticals Corp. (CA)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match           100.0%;  Score 15;  DB 6;  Length 15;
  Best Local Similarity  100.0%;  Pred. No. 1.2e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATGC 15
              |||||||||||||||
Db          1 GTGCTCCATTGATGC 15


RESULT 11
BD106498
LOCUS       BD106498                 15 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  High efficiency encapsulation of charged therapeutic agents in
            lipid vesicles.
ACCESSION   BD106498
VERSION     BD106498.1  GI:23201316
KEYWORDS    JP 2002501511-A/15.
SOURCE      Chlamydia sp.
  ORGANISM  Chlamydia sp.
            Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Semple,S.C., Klimuk,S.K., Harasym,T., Hope,M.J., Ansel,S.M.,
            Cullis,P., Scherrer,P. and Debeyer,D.S.
  TITLE     High efficiency encapsulation of charged therapeutic agents in
            lipid vesicles
  JOURNAL   Patent: JP 2002501511-A 15 15-JAN-2002;
            INEX PHARMACEUTICALS CORP
COMMENT     PN   JP 2002501511-A/15
            PD   15-JAN-2002
            PF   14-MAY-1998 JP 1998548646
            PI   SEAN C SEMPLE,SANDRA K KLIMUK,TROY HARASYM,MICHAEL J HOPE, PI
             STEVEN M ANSELL,
            PI   PIETER CULLIS,PETER SCHERRER,DAN SUITE DEBEYER PC   A61K9/00
            CC   Strandedness: Single;
```

```
          CC   Topology: Linear;
          FH   Key             Location/Qualifiers.
FEATURES              Location/Qualifiers
     source           1. .15
                      /organism="Chlamydia sp."
                      /mol_type="genomic DNA"
                      /db_xref="taxon:35827"
ORIGIN

  Query Match             100.0%;  Score 15;  DB 6;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATGC 15
              |||||||||||||||
Db          1 GTGCTCCATTGATGC 15


RESULT 12
AR073978
LOCUS       AR073978                 20 bp    DNA     linear   PAT 28-AUG-2000
DEFINITION  Sequence 47 from patent US 5952229.
ACCESSION   AR073978
VERSION     AR073978.1  GI:10000738
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Monia,B.P. and Boggs,R.T.
  TITLE     Antisense oligonucleotide modulation of raf gene expression
  JOURNAL   Patent: US 5952229-A 47 14-SEP-1999;
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="unknown"
                      /mol_type="unassigned DNA"
ORIGIN

  Query Match             100.0%;  Score 15;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATGC 15
              |||||||||||||||
Db          5 GTGCTCCATTGATGC 19


RESULT 13
AR216002
LOCUS       AR216002                 20 bp    DNA     linear   PAT 25-SEP-2002
DEFINITION  Sequence 49 from patent US 6410518.
ACCESSION   AR216002
VERSION     AR216002.1  GI:23314290
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Monia,B.P.
  TITLE     Antisense oligonucleotide inhibition of raf gene expression
  JOURNAL   Patent: US 6410518-A 49 25-JUN-2002;
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="unknown"
                      /mol_type="genomic DNA"
ORIGIN

  Query Match             100.0%;  Score 15;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATGC 15
              |||||||||||||||
Db          5 GTGCTCCATTGATGC 19


RESULT 14
AR110776
LOCUS       AR110776                 25 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 2 from patent US 6126965.
ACCESSION   AR110776
VERSION     AR110776.1  GI:12827624
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Kasid,U., Gokhale,P., Dritschilo,A. and Rahman,A.
  TITLE     Liposomes containing oligonucleotides
  JOURNAL   Patent: US 6126965-A 2 03-OCT-2000;
FEATURES              Location/Qualifiers
     source           1. .25
                      /organism="unknown"
                      /mol_type="unassigned DNA"
ORIGIN

  Query Match             100.0%;  Score 15;  DB 6;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATGC 15
              |||||||||||||||
Db          8 GTGCTCCATTGATGC 22


RESULT 15
AR310686
LOCUS       AR310686                 25 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 2 from patent US 6559129.
ACCESSION   AR310686
VERSION     AR310686.1  GI:31703830
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Kasid,U., Gokhale,P., Zhang,C., Dritschilo,A. and Rahman,A.
  TITLE     Cationic liposomal delivery system and therapeutic use thereof
  JOURNAL   Patent: US 6559129-A 2 06-MAY-2003;
FEATURES              Location/Qualifiers
     source           1. .25
                      /organism="unknown"
                      /mol_type="genomic DNA"
ORIGIN

  Query Match             100.0%;  Score 15;  DB 6;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATGC 15
              |||||||||||||||
Db          8 GTGCTCCATTGATGC 22


Search completed: June 21, 2005, 06:00:54
Job time : 1689 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 21, 2005, 06:01:03 ; Search time 6157 Seconds
(without alignments)
15.123 Million cell updates/sec

Title: US-10-075-994A-1
Perfect score: 15
Sequence: 1 gtgctccattgatgc 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6054689 seqs, 3103772919 residues

Total number of hits satisfying chosen parameters: 6057884

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
19: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq:*
20: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq:*
21: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq:*
22: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
23: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq:*
24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	15	100.0	15	9	US-09-930-283A-1	Sequence 1, Appli
c	2	15	100.0	15	9	US-09-930-283A-3	Sequence 3, Appli
	3	15	100.0	15	10	US-09-895-480A-15	Sequence 15, Appl
	4	15	100.0	15	15	US-10-290-545-25	Sequence 25, Appl
	5	15	100.0	15	16	US-10-365-623-16	Sequence 16, Appl
	6	15	100.0	15	17	US-10-075-994A-1	Sequence 1, Appli
c	7	15	100.0	15	17	US-10-075-994A-3	Sequence 3, Appli
	8	15	100.0	15	17	US-10-075-994A-4	Sequence 4, Appli
	9	15	100.0	15	17	US-10-347-924-1	Sequence 1, Appli
	10	15	100.0	15	17	US-10-437-263-25	Sequence 25, Appl
	11	15	100.0	15	17	US-10-437-275-25	Sequence 25, Appl
	12	15	100.0	15	17	US-10-437-258-25	Sequence 25, Appl
	13	15	100.0	15	21	US-10-925-734-15	Sequence 15, Appl
	14	15	100.0	20	14	US-10-057-550-49	Sequence 49, Appl
	15	15	100.0	20	15	US-10-173-225B-47	Sequence 47, Appl
	16	15	100.0	25	9	US-09-930-283A-2	Sequence 2, Appli
	17	15	100.0	25	17	US-10-075-994A-2	Sequence 2, Appli
c	18	15	100.0	25	21	US-10-809-189-113549	Sequence 113549,
c	19	15	100.0	25	21	US-10-809-189-113550	Sequence 113550,
c	20	14	93.3	25	21	US-10-809-189-113548	Sequence 113548,
c	21	13.4	89.3	25	21	US-10-719-900-817261	Sequence 817261,
	22	13	86.7	20	14	US-10-057-550-2	Sequence 2, Appli
	23	13	86.7	20	15	US-10-173-225B-2	Sequence 2, Appli
	24	13	86.7	25	21	US-10-719-900-495729	Sequence 495729,
c	25	12.4	82.7	20	8	US-08-731-499-19	Sequence 19, Appl
	26	12.4	82.7	21	17	US-10-321-039-657	Sequence 657, App
	27	12.4	82.7	25	21	US-10-719-900-12019	Sequence 12019, A
c	28	12.4	82.7	25	21	US-10-719-900-59921	Sequence 59921, A
	29	12.4	82.7	25	21	US-10-719-900-61852	Sequence 61852, A
	30	12.4	82.7	25	21	US-10-719-900-177397	Sequence 177397,
c	31	12.4	82.7	25	21	US-10-719-900-227769	Sequence 227769,
	32	12.4	82.7	25	21	US-10-719-900-272122	Sequence 272122,
c	33	12.4	82.7	25	21	US-10-719-900-357986	Sequence 357986,
	34	12.4	82.7	25	21	US-10-719-900-781945	Sequence 781945,
c	35	12.4	82.7	25	21	US-10-809-189-36748	Sequence 36748, A
c	36	12.4	82.7	25	21	US-10-809-189-36749	Sequence 36749, A
	37	12.4	82.7	25	21	US-10-809-189-127169	Sequence 127169,
c	38	12.4	82.7	25	21	US-10-809-189-127433	Sequence 127433,
c	39	12.4	82.7	25	21	US-10-809-189-127444	Sequence 127444,
c	40	12	80.0	20	13	US-10-078-949-5	Sequence 5, Appli
	41	12	80.0	20	14	US-10-057-550-3	Sequence 3, Appli
c	42	12	80.0	20	14	US-10-280-600-5	Sequence 5, Appli
	43	12	80.0	20	14	US-10-280-600-6	Sequence 6, Appli
c	44	12	80.0	20	14	US-10-281-312-5	Sequence 5, Appli
	45	12	80.0	20	14	US-10-281-312-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-09-930-283A-1
; Sequence 1, Application US/09930283A
; Patent No. US20020160038A1
; GENERAL INFORMATION:
; APPLICANT: Kasid, Usha
; Gokhale, Prafulla
; Dritschilo, Anatoly
; Rahman, Aqulur
; TITLE OF INVENTION: Liposomes contaiing Oligonucelotides
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hendricks and Assoc.
; STREET: P.O. Box 2509
; CITY: Fairfax
; STATE: VA
; COUNTRY: US
; ZIP: 22031
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/930,283A
; FILING DATE: 16-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/354,109
; FILING DATE: 1999-07-15

```
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Hendricks, Glenna
;            REGISTRATION NUMBER: 32,535
;            REFERENCE/DOCKET NUMBER: kasid
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (703) 591-4470
;            TELEFAX: (703) 591-4428
;   INFORMATION FOR SEQ ID NO: 1:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 15 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: unknown
;       MOLECULE TYPE: DNA (genomic)
;       HYPOTHETICAL: NO
;       ANTI-SENSE: YES
;       SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-930-283A-1

  Query Match             100.0%;  Score 15;  DB 9;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATGC 15
              |||||||||||||||
Db          1 GTGCTCCATTGATGC 15


RESULT 2
US-09-930-283A-3/c
; Sequence 3, Application US/09930283A
; Patent No. US20020160038A1
;   GENERAL INFORMATION:
;       APPLICANT: Kasid, Usha
;                  Gokhale, Prafulla
;                  Dritschilo, Anatoly
;                  Rahman, Aqulur
;       TITLE OF INVENTION: Liposomes contaiing Oligonucelotides
;       NUMBER OF SEQUENCES: 3
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Hendricks and Assoc.
;            STREET: P.O. Box 2509
;            CITY: Fairfax
;            STATE: VA
;            COUNTRY: US
;            ZIP: 22031
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/930,283A
;            FILING DATE: 16-Aug-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/354,109
;            FILING DATE: 1999-07-15
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Hendricks, Glenna
;            REGISTRATION NUMBER: 32,535
;            REFERENCE/DOCKET NUMBER: kasid
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (703) 591-4470
;            TELEFAX: (703) 591-4428
;   INFORMATION FOR SEQ ID NO: 3:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 15 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: unknown
;       MOLECULE TYPE: DNA (genomic)
;       HYPOTHETICAL: NO
;       ANTI-SENSE: YES
;       SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-930-283A-3

  Query Match             100.0%;  Score 15;  DB 9;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATGC 15
              |||||||||||||||
Db         15 GTGCTCCATTGATGC 1


RESULT 3
US-09-895-480A-15
; Sequence 15, Application US/09895480A
; Publication No. US20030129221A1
;   GENERAL INFORMATION:
;       APPLICANT: Inex Pharmaceuticals Inc.
;       TITLE OF INVENTION: High Efficiency Encapsulation of Charged Therapeutic
;                           Agents in
;                           Lipid Vesicles
;       NUMBER OF SEQUENCES: 17
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Oppedahl & Larson LLP
;            STREET: PO Box 5068
;            CITY: Dillon
;            STATE: CO
;            COUNTRY: US
;            ZIP: 80435
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
;            COMPUTER: IBM Compatible
;            OPERATING SYSTEM: DOS 5.0
;            SOFTWARE: Word Perfect
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/895,480A
;            FILING DATE: 29-Jun-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: <Unknown>
;            FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: <Unknown>
;            REGISTRATION NUMBER: <Unknown>
;            REFERENCE/DOCKET NUMBER: <Unknown>
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: <Unknown>
;            TELEFAX: <Unknown>
;            TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 15:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 15
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: other nucleic acid
;       HYPOTHETICAL: no
;       ANTI-SENSE: yes
;       SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-895-480A-15

  Query Match             100.0%;  Score 15;  DB 10;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATGC 15
              |||||||||||||||
Db          1 GTGCTCCATTGATGC 15


RESULT 4
US-10-290-545-25
```

```
; Sequence 25, Application US/10290545
; Publication No. US20030125292A1
; GENERAL INFORMATION:
;  APPLICANT: Semple, Sean
;  APPLICANT:  Klimuk, Sandy
;  APPLICANT:  Yuan, Zuan-Ning
;  TITLE OF INVENTION: Improved Mucosal Vaccines and Methods for Using the Same
;  FILE REFERENCE: A-71854/TAL/AXG
;  CURRENT APPLICATION NUMBER: US/10/290,545
;  CURRENT FILING DATE:  2002-11-07
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-290-545-25

  Query Match           100.0%;  Score 15;  DB 15;  Length 15;
  Best Local Similarity  100.0%;  Pred. No. 1.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATGC 15
              |||||||||||||||
Db          1 GTGCTCCATTGATGC 15


RESULT 5
US-10-365-623-16
; Sequence 16, Application US/10365623
; Publication No. US20030166512A1
; GENERAL INFORMATION:
;  APPLICANT: Xie, Dong
;  TITLE OF INVENTION: Protein Carrier System for Therapeutic Oligonucleotides
;  FILE REFERENCE: 63024.000001
;  CURRENT APPLICATION NUMBER: US/10/365,623
;  CURRENT FILING DATE:  2003-02-13
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense oligonucleotide directed against human c-raf-1 protein
;   OTHER INFORMATION: kinase
US-10-365-623-16

  Query Match           100.0%;  Score 15;  DB 16;  Length 15;
  Best Local Similarity  100.0%;  Pred. No. 1.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATGC 15
              |||||||||||||||
Db          1 GTGCTCCATTGATGC 15


RESULT 6
US-10-075-994A-1
; Sequence 1, Application US/10075994A
; Publication No. US20030215489A1
; GENERAL INFORMATION:
;  APPLICANT: KASID, Usha
;  APPLICANT:  GOKHALE, Prafulla
;  APPLICANT:  PIE, Jin
;  APPLICANT:  MEWANI, Rajshree
;  APPLICANT:  AHMAD, Imran
;  APPLICANT:  DRITSCHILO, Anatoly
;  APPLICANT:  RAHMAN, Aquilur
;  TITLE OF INVENTION: CHEMOSENSITIZING WITH LIPOSOMES CONTAINING OLIGONUCLEOTIDES
;  FILE REFERENCE: 219604
;  CURRENT APPLICATION NUMBER: US/10/075,994A
;  CURRENT FILING DATE:  2002-02-15
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic
US-10-075-994A-1

  Query Match           100.0%;  Score 15;  DB 17;  Length 15;
  Best Local Similarity  100.0%;  Pred. No. 1.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATGC 15
              |||||||||||||||
Db          1 GTGCTCCATTGATGC 15


RESULT 7
US-10-075-994A-3/c
; Sequence 3, Application US/10075994A
; Publication No. US20030215489A1
; GENERAL INFORMATION:
;  APPLICANT: KASID, Usha
;  APPLICANT:  GOKHALE, Prafulla
;  APPLICANT:  PIE, Jin
;  APPLICANT:  MEWANI, Rajshree
;  APPLICANT:  AHMAD, Imran
;  APPLICANT:  DRITSCHILO, Anatoly
;  APPLICANT:  RAHMAN, Aquilur
;  TITLE OF INVENTION: CHEMOSENSITIZING WITH LIPOSOMES CONTAINING OLIGONUCLEOTIDES
;  FILE REFERENCE: 219604
;  CURRENT APPLICATION NUMBER: US/10/075,994A
;  CURRENT FILING DATE:  2002-02-15
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic
US-10-075-994A-3

  Query Match           100.0%;  Score 15;  DB 17;  Length 15;
  Best Local Similarity  100.0%;  Pred. No. 1.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATGC 15
              |||||||||||||||
Db         15 GTGCTCCATTGATGC 1


RESULT 8
US-10-075-994A-4
; Sequence 4, Application US/10075994A
; Publication No. US20030215489A1
; GENERAL INFORMATION:
;  APPLICANT: KASID, Usha
;  APPLICANT:  GOKHALE, Prafulla
;  APPLICANT:  PIE, Jin
;  APPLICANT:  MEWANI, Rajshree
;  APPLICANT:  AHMAD, Imran
;  APPLICANT:  DRITSCHILO, Anatoly
;  APPLICANT:  RAHMAN, Aquilur
;  TITLE OF INVENTION: CHEMOSENSITIZING WITH LIPOSOMES CONTAINING OLIGONUCLEOTIDES
;  FILE REFERENCE: 219604
;  CURRENT APPLICATION NUMBER: US/10/075,994A
;  CURRENT FILING DATE:  2002-02-15
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
```

; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-075-994A-4

  Query Match 100.0%; Score 15; DB 17; Length 15;
  Best Local Similarity 100.0%; Pred. No. 1.3e+02;
  Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCTCCATTGATGC 15
    ||||||||||||||
Db 1 GTGCTCCATTGATGC 15

RESULT 9
US-10-347-924-1
; Sequence 1, Application US/10347924
; Publication No. US20030229040A1
; GENERAL INFORMATION:
; APPLICANT: Kasid, Usha
; APPLICANT: Gokhale, Prafulla
; APPLICANT: Zhang, Chuanbo
; APPLICANT: Dristschilo, Anatoly
; APPLICANT: Rahman, Aquilur
; TITLE OF INVENTION: CATIONIC LIPOSOMAL DELIVERY SYSTEM AND THERAPEUTIC USE THEREOF
; FILE REFERENCE: 220807
; CURRENT APPLICATION NUMBER: US/10/347,924
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US 09/354,109
; PRIOR FILING DATE: 1999-07-15
; PRIOR APPLICATION NUMBER: US 08/957,327
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: US 60/041,192
; PRIOR FILING DATE: 1997-03-21
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-10-347-924-1

  Query Match 100.0%; Score 15; DB 17; Length 15;
  Best Local Similarity 100.0%; Pred. No. 1.3e+02;
  Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCTCCATTGATGC 15
    ||||||||||||||
Db 1 GTGCTCCATTGATGC 15

RESULT 10
US-10-437-263-25
; Sequence 25, Application US/10437263
; Publication No. US20040009943A1
; GENERAL INFORMATION:
; APPLICANT: Semple, Sean
; APPLICANT: Tam, Ying K.
; APPLICANT: Chikh, Ghania
; APPLICANT: Hope, Michael J.
; TITLE OF INVENTION: PATHOGEN VACCINES AND METHODS FOR USING THE SAME
; FILE REFERENCE: A-72216/TAL
; CURRENT APPLICATION NUMBER: US/10/437,263
; CURRENT FILING DATE: 2003-05-12
; PRIOR APPLICATION NUMBER: 60/379,343
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: 60/460,646
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 60/454,298
; PRIOR FILING DATE: 2003-03-12
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-437-263-25

  Query Match 100.0%; Score 15; DB 17; Length 15;
  Best Local Similarity 100.0%; Pred. No. 1.3e+02;
  Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCTCCATTGATGC 15
    ||||||||||||||
Db 1 GTGCTCCATTGATGC 15

RESULT 11
US-10-437-275-25
; Sequence 25, Application US/10437275
; Publication No. US20040009944A1
; GENERAL INFORMATION:
; APPLICANT: Tam, Ying K.
; APPLICANT: Semple, Sean
; APPLICANT: Klimuk, Sandra
; APPLICANT: Chikh, Ghania
; TITLE OF INVENTION: METHYLATED IMMUNOSTIMULATORY OLIGONUCLEOTIDES AND METHODS OF
; TITLE OF INVENTION: USING THE SAME
; FILE REFERENCE: A-72158/TAL
; CURRENT APPLICATION NUMBER: US/10/437,275
; CURRENT FILING DATE: 2003-05-12
; PRIOR APPLICATION NUMBER: 60/379,343
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: 60/460,646
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/290,545
; PRIOR FILING DATE: 2002-11-07
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-437-275-25

  Query Match 100.0%; Score 15; DB 17; Length 15;
  Best Local Similarity 100.0%; Pred. No. 1.3e+02;
  Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCTCCATTGATGC 15
    ||||||||||||||
Db 1 GTGCTCCATTGATGC 15

RESULT 12
US-10-437-258-25
; Sequence 25, Application US/10437258
; Publication No. US20040013649A1
; GENERAL INFORMATION:
; APPLICANT: Tam, Ying K.
; APPLICANT: Semple, Sean
; APPLICANT: Klimuk, Sandra
; APPLICANT: Chikh, Ghania
; TITLE OF INVENTION: CANCER VACCINES AND METHODS OF USING THE SAME
; FILE REFERENCE: A-72252/TAL
; CURRENT APPLICATION NUMBER: US/10/437,258
; CURRENT FILING DATE: 2003-05-12
; PRIOR APPLICATION NUMBER: 60/379,343
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: 60/460,646
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 60/454,298

```
;  PRIOR FILING DATE: 2003-03-12
;  NUMBER OF SEQ ID NOS: 34
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-437-258-25

  Query Match           100.0%;  Score 15;  DB 17;  Length 15;
  Best Local Similarity  100.0%;  Pred. No. 1.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATGC 15
              |||||||||||||||
Db          1 GTGCTCCATTGATGC 15


RESULT 13
US-10-925-734-15
; Sequence 15, Application US/10925734
; Publication No. US20050008689A1
;   GENERAL INFORMATION:
;        APPLICANT: Inex Pharmaceuticals Inc.
;        TITLE OF INVENTION: High Efficiency Encapsulation of Charged
;                            Therapeutic
;                            Agents in
;                            Lipid Vesicles
;        NUMBER OF SEQUENCES: 17
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Oppedahl & Larson LLP
;             STREET: PO Box 5068
;             CITY: Dillon
;             STATE: CO
;             COUNTRY: US
;             ZIP: 80435
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS 5.0
;             SOFTWARE: Word Perfect
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/925,734
;             FILING DATE: 24-Aug-2004
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/895,480
;             FILING DATE: 29-Jun-2001
;        ATTORNEY/AGENT INFORMATION:
;             NAME: <Unknown>
;             REGISTRATION NUMBER: <Unknown>
;             REFERENCE/DOCKET NUMBER: <Unknown>
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: <Unknown>
;             TELEFAX: <Unknown>
;             TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 15:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 15
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: other nucleic acid
;        HYPOTHETICAL: no
;        ANTI-SENSE: yes
;        SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-10-925-734-15

  Query Match           100.0%;  Score 15;  DB 21;  Length 15;
  Best Local Similarity  100.0%;  Pred. No. 1.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATGC 15
              |||||||||||||||
Db          1 GTGCTCCATTGATGC 15


RESULT 14
US-10-057-550-49
; Sequence 49, Application US/10057550
; Publication No. US20030032607A1
; GENERAL INFORMATION:
;  APPLICANT: Monia, Brett P.
;  TITLE OF INVENTION: Antisense Oligonucleotide Modulation of raf Gene Expression
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/10/057,550
;  CURRENT FILING DATE:  2002-01-25
;  PRIOR APPLICATION NUMBER: 09/506,073
;  PRIOR FILING DATE: 2000-02-18
;  PRIOR APPLICATION NUMBER: US 09/143,214
;  PRIOR FILING DATE: 1998-08-28
;  PRIOR APPLICATION NUMBER: PCT/US98/13961
;  PRIOR FILING DATE: 1998-07-06
;  PRIOR APPLICATION NUMBER: US 08/888,982
;  PRIOR FILING DATE: 1997-07-07
;  PRIOR APPLICATION NUMBER: US 08/756,806
;  PRIOR FILING DATE: 1996-11-26
;  PRIOR APPLICATION NUMBER: PCT/US95/07111
;  PRIOR FILING DATE: 1995-05-31
;  PRIOR APPLICATION NUMBER: US 08/250,856
;  PRIOR FILING DATE: 1994-05-31
;  NUMBER OF SEQ ID NOS: 130
; SEQ ID NO 49
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: artificial sequence
;   FEATURE:
;   OTHER INFORMATION: antisense sequence
US-10-057-550-49

  Query Match           100.0%;  Score 15;  DB 14;  Length 20;
  Best Local Similarity  100.0%;  Pred. No. 1.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATGC 15
              |||||||||||||||
Db          5 GTGCTCCATTGATGC 19


RESULT 15
US-10-173-225B-47
; Sequence 47, Application US/10173225B
; Publication No. US20030119769A1
; GENERAL INFORMATION:
;  APPLICANT: Monia, Brett P.
;  TITLE OF INVENTION: Antisense Oligonucleotide Modulation of raf Gene Expression
;  FILE REFERENCE: ISPH-0665
;  CURRENT APPLICATION NUMBER: US/10/173,225B
;  CURRENT FILING DATE:  2002-12-06
;  PRIOR APPLICATION NUMBER: US 10/057,550
;  PRIOR FILING DATE: 2002-01-25
;  PRIOR APPLICATION NUMBER: US 09/143,214
;  PRIOR FILING DATE: 1998-08-28
;  PRIOR APPLICATION NUMBER: PCT/US98/13961
;  PRIOR FILING DATE: 1998-07-06
;  PRIOR APPLICATION NUMBER: US 08/888,982
;  PRIOR FILING DATE: 1997-07-07
;  PRIOR APPLICATION NUMBER: US 08/756,806
;  PRIOR FILING DATE: 1996-11-26
;  PRIOR APPLICATION NUMBER: PCT/US95/07111
;  PRIOR FILING DATE: 1995-05-31
;  PRIOR APPLICATION NUMBER: US 08/250,856
;  PRIOR FILING DATE: 1994-05-31
;  NUMBER OF SEQ ID NOS: 109
; SEQ ID NO 47
;   LENGTH: 20
```

; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-10-173-225B-47

  Query Match 100.0%; Score 15; DB 15; Length 20;
  Best Local Similarity 100.0%; Pred. No. 1.3e+02;
  Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GTGCTCCATTGATGC 15
              |||||||||||||||
Db          5 GTGCTCCATTGATGC 19
```

Search completed: June 21, 2005, 11:35:23
Job time : 6157 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: June 21, 2005, 05:02:47 ; Search time 2999 Seconds
(without alignments)
190.385 Million cell updates/sec

Title: US-10-075-994A-1
Perfect score: 15
Sequence: 1 gtgctccattgatgc 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 159776

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	12.4	82.7	40	1	AA434107	AA434107 zw24b01.s
c	2	12.4	82.7	41	9	CL213712	A037F07 G
c	3	12.4	82.7	41	9	CW509288	CW509288 BGA434 Ba
c	4	12.4	82.7	43	9	CC894144	CC894144 RRK138 Ba
c	5	12.4	82.7	47	8	CC200383	CC200383 RRE120 Ba
c	6	11.8	78.7	32	9	CL659092	CL659092 PRI0133a_
	7	11	73.3	27	9	AG190569	AG190569 Pan trogl
	8	11	73.3	39	8	AZ579181	AZ579181 1M0363G10
	9	11	73.3	46	9	CL982908	CL982908 GC0134 TI
c	10	11	73.3	49	9	BX659267	BX659267 Arabidops
	11	10.8	72.0	26	8	AZ769902	AZ769902 1M0571G06
c	12	10.8	72.0	28	1	AU256788	AU256788 AU256788
c	13	10.8	72.0	28	8	AZ780454	AZ780454 2M0017O16
c	14	10.8	72.0	42	9	TA59H06P	AL455680 T. brucei
	15	10.8	72.0	43	7	CV521218	CV521218 0089P0056
	16	10.8	72.0	43	9	CL256795	CL256795 XT0290 Sa
c	17	10.8	72.0	45	8	AZ317769	AZ317769 1M0036O02
	18	10.8	72.0	46	1	AI941313	AI941313 sb87e01.y
c	19	10.8	72.0	47	7	CF339432	CF339432 RCL1--04-
c	20	10.8	72.0	49	1	AA444355	AA444355 vd92d04.r
	21	10.8	72.0	50	1	AJ558646	AJ558646 AJ558646
c	22	10.8	72.0	50	1	AU103457	AU103457 AU103457
c	23	10.8	72.0	50	6	CB226725	CB226725 1Ru29D04
	24	10.4	69.3	22	9	TA197A04Q	AL477173 T. brucei
c	25	10.4	69.3	23	8	AZ760244	AZ760244 1M0553C19
c	26	10.4	69.3	30	8	BZ596965	BZ596965 SALK_0979
	27	10.4	69.3	31	9	AG199008	AG199008 Pan trogl
c	28	10.4	69.3	34	8	AZ786136	AZ786136 1M0031M21
	29	10.4	69.3	38	8	BZ664429	BZ664429 SALK_0711
	30	10.4	69.3	44	9	CG781920	CG781920 1123047D1
	31	10.4	69.3	49	1	AI035265	AI035265 ue18b08.x
	32	10.4	69.3	49	1	AI888465	AI888465 wn32a07.x
	33	10.4	69.3	49	8	BH852072	BH852072 SALK_0741
c	34	10.4	69.3	49	9	BX654661	BX654661 Arabidops
c	35	10.2	68.0	26	8	AZ308069	AZ308069 1M0010N09
c	36	10.2	68.0	27	8	AZ991985	AZ991985 2M0276P21
	37	10.2	68.0	33	4	BJ060580	BJ060580 BJ060580
	38	10.2	68.0	34	8	CC049952	CC049952 01S0530-0
	39	10.2	68.0	35	8	AZ654998	AZ654998 1M0529L12
c	40	10.2	68.0	35	9	CG785587	CG785587 00S0119-0
c	41	10.2	68.0	40	1	AI900047	AI900047 sb98b08.y
	42	10.2	68.0	41	9	AL946655	AL946655 Arabidops
c	43	10.2	68.0	43	1	AI426076	AI426076 mh31h05.x
	44	10.2	68.0	43	1	AV833106	AV833106 AV833106
c	45	10.2	68.0	43	4	BJ001161	BJ001161 BJ001161

ALIGNMENTS

RESULT 1
AA434107/c
LOCUS AA434107 40 bp mRNA linear EST 29-MAY-1997
DEFINITION zw24b01.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:770185 3' similar to TR:G556217 G556217 SPLICEOSOMAL PROTEIN. ;, mRNA sequence.
ACCESSION AA434107
VERSION AA434107.1 GI:2139021
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 40)
AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
TITLE WashU-Merck EST Project 1997
JOURNAL Unpublished (1997)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -41m13 fwd. ET from Amersham
High quality sequence stop: 1.
FEATURES Location/Qualifiers
source 1. .40
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:5980060"
/db_xref="taxon:9606"
/clone="IMAGE:770185"
/sex="Female"
/tissue_type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares ovary tumor NbHOT"
/note="Organ: ovary; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGGCCGCGGTTTTTTTTTTTTTTTTTT 3'],

double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo. "
ORIGIN

Query Match 82.7%; Score 12.4; DB 1; Length 40;
Best Local Similarity 92.9%; Pred. No. 2e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TGCTCCATTGATGC 15
| ||||||||||||
Db 17 TCCTCCATTGATGC 4

RESULT 2
CL213712/c
LOCUS CL213712 41 bp mRNA linear GSS 30-JUN-2004
DEFINITION A037F07 GGTC Gene Trap Library GV03C04 Mus musculus cDNA clone A037F07, mRNA sequence.
ACCESSION CL213712
VERSION CL213712.2 GI:49489570
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 41)
AUTHORS Hansen,J., Floss,T., van Sloun,P., Fuchtbauer,E.M., Vauti,F., Arnold,H.H., Schnutgen,F., Wurst,W., Von Melchner,H. and Ruiz,P.
TITLE A large-scale, gene-driven mutagenesis approach for the functional analysis of the mouse genome
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 100 (17), 9918-9922 (2003)
MEDLINE 22810117
PUBMED 12904583
COMMENT On Jun 30, 2004 this sequence version replaced gi:40730613.
Contact: GGTC
German Genetrap Consortium (GGTC)
Email: info@genetrap.de
pT1betageo gene trap. Sequence tag generated by 5'RACE. Additional sequence information can be found at:
'http://genetrap.gsf.de/project/web_new/database/result_clone.html?clone_id=A037F07' ES cell line harboring insertion mutation of target gene is available at:
'http://genetrap.gsf.de/project/web_new/order_clones/howtoorder.htm1' Inhouse Sequence Identifier: 09103
Class: Gene Trap.
FEATURES Location/Qualifiers
source 1. .41
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129 Sv"
/db_xref="taxon:10090"
/clone="A037F07"
/sex="Male"
/cell_type="Embryonic stem cell"
/cell_line="ES cells 129S2 (formerly 129/SvPas)"
/clone_lib="GGTC Gene Trap Library GV03C04"
/note="Vector: pT1betageo"
ORIGIN

Query Match 82.7%; Score 12.4; DB 9; Length 41;
Best Local Similarity 92.9%; Pred. No. 2e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TGCTCCATTGATGC 15
||||||||| ||||
Db 21 TGCTCCATTCATGC 8

RESULT 3
CW509288/c
LOCUS CW509288 41 bp mRNA linear GSS 06-OCT-2004
DEFINITION BGA434 BayGenomics Gene Trap Library pGT1Lxf Mus musculus cDNA, mRNA sequence.
ACCESSION CW509288
VERSION CW509288.1 GI:53838793
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 41)
AUTHORS BayGenomics.
TITLE http://baygenomics.ucsf.edu/
JOURNAL Unpublished (2001)
COMMENT Contact: BayGenomics
Bay Area Functional Genomics Consortium (BayGenomics)
Email: info@baygenomics.ucsf.edu
Sequence tag generated by 5' RACE of total RNA from gene trap ES cell line. ES cell lines harboring insertion mutation of target gene are available upon request from BayGenomics. Annotation information available from
http://baygenomics.ucsf.edu/cgi-bin/BaySearch.py?OPTION=EXACT&TYPE=CELL_LINE&KEY=BGA434
Class: Gene Trap.
FEATURES Location/Qualifiers
source 1. .41
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129 ola"
/db_xref="taxon:10090"
/sex="Male"
/cell_type="Embryonic stem cell"
/clone_lib="BayGenomics Gene Trap Library pGT1Lxf"
/note="Vector: pGT1Lxf"
ORIGIN

Query Match 82.7%; Score 12.4; DB 9; Length 41;
Best Local Similarity 92.9%; Pred. No. 2e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TGCTCCATTGATGC 15
||||||||| ||||
Db 24 TGCTCCATTCATGC 11

RESULT 4
CC894144/c
LOCUS CC894144 43 bp mRNA linear GSS 02-SEP-2003
DEFINITION RRK138 BayGenomics Gene Trap Library pGT2Lxf Mus musculus cDNA, mRNA sequence.
ACCESSION CC894144
VERSION CC894144.2 GI:34408991
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 43)
AUTHORS BayGenomics.
TITLE http://baygenomics.ucsf.edu/
JOURNAL Unpublished (2001)
COMMENT On Sep 2, 2003 this sequence version replaced gi:33392557.
Contact: BayGenomics
Bay Area Functional Genomics Consortium (BayGenomics)
Email: info@baygenomics.ucsf.edu
Sequence tag generated by 5' RACE of total RNA from gene trap ES cell line. ES cell lines harboring insertion mutation of target gene are available upon request from BayGenomics. Annotation information available from
http://baygenomics.ucsf.edu/cgi-bin/BaySearch.py?OPTION=EXACT&TYPE=CELL_LINE&KEY=RRK138
Class: Gene Trap.
FEATURES Location/Qualifiers

```
     source          1. .43
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="129 ola"
                     /db_xref="taxon:10090"
                     /sex="Male"
                     /cell_type="Embryonic stem cell"
                     /clone_lib="BayGenomics Gene Trap Library pGT2Lxf"
                     /note="Vector: pGT2Lxf"
ORIGIN

  Query Match             82.7%;  Score 12.4;  DB 9;  Length 43;
  Best Local Similarity   92.9%;  Pred. No. 2e+04;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 TGCTCCATTGATGC 15
              ||||||||| ||||
Db         26 TGCTCCATTCATGC 13


RESULT 5
CC200383/c
LOCUS       CC200383                 47 bp    mRNA    linear   GSS 09-MAY-2003
DEFINITION  RRE120 BayGenomics Gene Trap Library pGT2Lxf Mus musculus cDNA,
            mRNA sequence.
ACCESSION   CC200383
VERSION     CC200383.1  GI:30480146
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 47)
  AUTHORS   BayGenomics.
  TITLE     http://baygenomics.ucsf.edu/
  JOURNAL   Unpublished (2001)
COMMENT     Contact: BayGenomics
            Bay Area Functional Genomics Consortium (BayGenomics)
            Email: info@baygenomics.ucsf.edu
            Sequence tag generated by 5' RACE of total RNA from gene trap ES
            cell line. ES cell lines harboring insertion mutation of target
            gene are available upon request from BayGenomics. Annotation
            information available from
            http://baygenomics.ucsf.edu/cgi-bin/BaySearch.py?OPTION=EXACT&TYPE=
            CELL_LINE&KEY=RRE120
            Class: Gene Trap.
FEATURES             Location/Qualifiers
     source          1. .47
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="129 ola"
                     /db_xref="taxon:10090"
                     /sex="Male"
                     /cell_type="Embryonic stem cell"
                     /clone_lib="BayGenomics Gene Trap Library pGT2Lxf"
                     /note="Vector: pGT2Lxf"
ORIGIN

  Query Match             82.7%;  Score 12.4;  DB 8;  Length 47;
  Best Local Similarity   92.9%;  Pred. No. 2.1e+04;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 TGCTCCATTGATGC 15
              ||||||||| ||||
Db         30 TGCTCCATTCATGC 17


RESULT 6
CL659092/c
LOCUS       CL659092                 32 bp    DNA     linear   GSS 09-JUL-2004
DEFINITION  PRI0133a_G11 - PRI0133a.B21.1 (32) Mixed stage fosmid library of P.
            pacificus var. California Pristionchus pacificus genomic, genomic
            survey sequence.
ACCESSION   CL659092
VERSION     CL659092.1  GI:50142802
KEYWORDS    GSS.
SOURCE      Pristionchus pacificus
  ORGANISM  Pristionchus pacificus
            Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
            Neodiplogasteridae; Pristionchus.
REFERENCE   1  (bases 1 to 32)
  AUTHORS   Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
  TITLE     AppaDB: an AcedB database for the nematode satellite organism
            Pristionchus pacificus
  JOURNAL   Nucleic Acids Res. 32 (1), D421-D422 (2004)
COMMENT     Contact: Sommer RJ
            Evolutionary Biology
            Max-Planck-Institute for Developmental Biology
            Spemannstr. 37-39, Tuebingen D-72076, Germany
            Tel: 00497071601371
            Fax: 00497071601498
            Email: ralf.sommer@tuebingen.mpg.de
            This library was generated at Caltech, Pasadena, USA and end
            sequenced at Vancouver, Canada.
            Seq primer: T7
            Class: fosmid ends.
FEATURES             Location/Qualifiers
     source          1. .32
                     /organism="Pristionchus pacificus"
                     /mol_type="genomic DNA"
                     /strain="California"
                     /db_xref="taxon:54126"
                     /clone_lib="Mixed stage fosmid library of P. pacificus
                     var. California"
                     /note="Vector: pEpifos-5 Fosmid vector"
ORIGIN

  Query Match             78.7%;  Score 11.8;  DB 9;  Length 32;
  Best Local Similarity   86.7%;  Pred. No. 4.4e+04;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATGC 15
              |||||||| |||| |
Db         29 GTGCTCCACTGATCC 15


RESULT 7
AG190569
LOCUS       AG190569                 27 bp    DNA     linear   GSS 06-MAR-2004
DEFINITION  Pan troglodytes DNA, clone: RP43-066B21.TJ, genomic survey
            sequence.
ACCESSION   AG190569
VERSION     AG190569.1  GI:45222745
KEYWORDS    GSS.
SOURCE      Pan troglodytes (chimpanzee)
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE   1
  AUTHORS   Park,H., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Eun,C.J.,
            Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.
  TITLE     BAC end sequences of Library RP-43
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 27)
  AUTHORS   Park,H., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Eun,C.J.,
            Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of
            Bioscience and Biotechnology (KRIBB), Genome Research Center (GRC);
            52, Oun-dong, Yusong-gu, Daejeon 305-333, Korea
            (E-mail:redstone@mail.kribb.re.kr, URL:http://phs.grc.kribb.re.kr/,
            Tel:82-42-866-7181, Fax:82-42-860-4409)
COMMENT     Clones are derived from the chimpanzee BAC library RP-43 This BAC
            end was generated during the R&D process and may have higher chance
            of clone tracking errors.
             PRIMERS
```

```
            Sequencing: TJ
          LIBRARY
            Vector    : pBACe3.6
            R.Site 1  : EcoRI
            R.Site 2  : EcoRI.
FEATURES            Location/Qualifiers
     source         1. .27
                    /organism="Pan troglodytes"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:9598"
                    /clone="RP43-066B21.TJ"
                    /sex="male"
                    /cell_type="lymphocytes"
                    /clone_lib="RP-43 Chimpanzee Male BAC Library"
ORIGIN

  Query Match             73.3%;  Score 11;  DB 9;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTG 11
              ||||||||||| |
Db         16 GTGCTCCATTG 26


RESULT 8
AZ579181
LOCUS       AZ579181                 39 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  1M0363G10F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0363G10 F, genomic survey sequence.
ACCESSION   AZ579181
VERSION     AZ579181.1  GI:11693526
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 39)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0363  row: G  column: 10
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 39.
FEATURES            Location/Qualifiers
     source         1. .39
                    /organism="Mus musculus"
                    /mol_type="genomic DNA"
                    /strain="C57BL/6J"
                    /db_xref="taxon:10090"
                    /clone="UUGC1M0363G10"
                    /sex="Male"
                    /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                    /clone_lib="Mouse 10kb plasmid UUGC1M library"
                    /note="Vector: PWD42nv; Purified genomic DNA from M.
                    musculus C57BL/6J (male) was obtained  from the Jackson
                    Laboratory Mouse DNA Resource
                    (http://www.jax.org/resources/documents/dnares/). The DNA
                    was hydrodynamically sheared by repeated passage through a
                    0.005 inch orifice at constant velocity. The sheared DNA
                    was blunt end-repaired with T4 DNA polymerase and T4
                    polynucleotide kinase. Adaptor oligonucleotides were
                    ligated to the blunt ends in high  molar excess. The
                    adaptored DNA was purified and size-selected for a 9.5 to
                    10.5 kb range using preparative agarose gel
                    electrophoresis. Vector DNA was prepared from a derivative
                    of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                    inducible derivative of plasmid R1. The vector was ligated
                    with adaptors complementary to the insert adaptors and
                    purified. The sheared, adaptored mouse DNA was annealed to
                    adaptored vector DNA, and transformed into
                    chemically-competent E. coli XL10-Gold (Stratagene) cells
                    and selected for ampicillin resistance."
ORIGIN

  Query Match             73.3%;  Score 11;  DB 8;  Length 39;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+05;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 TCCATTGATGC 15
              |||||||||||
Db         18 TCCATTGATGC 28


RESULT 9
CL982908
LOCUS       CL982908                 46 bp    mRNA    linear   GSS 21-SEP-2004
DEFINITION  GC0134 TIGEM gene trap library Mus musculus cDNA clone 8644.24,
            mRNA sequence.
ACCESSION   CL982908
VERSION     CL982908.1  GI:52420303
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 46)
  AUTHORS   Cobellis,G., Nicolaus,G., Marra,E., Barbarisi,M., Sardiello,M., Di
            Giorgio,F.P., Iovino,N., Zollo,M., Ballabio,A. and Cortese,R.
  TITLE     Tagging genes with cassette-exchange sites
  JOURNAL   Unpublished (2004)
COMMENT     Contact: TIGEM
            107
            TIGEM
            Via P. Castellino, 111, 80131 NAPOLI, ITALY
            Tel: +390816132205
            Fax: +390815790919
            Email: cobellis@tigem.it
            Sequence tag generated by 5' RACE of total RNA from gene trap ES
            cell line. ES cell lines harboring insertion mutation of target
            gene are available upon request from TIGEM. Annotation information
            available from TIGEM
            Class: Gene Trap.
FEATURES            Location/Qualifiers
     source         1. .46
                    /organism="Mus musculus"
                    /mol_type="mRNA"
                    /strain="129 ola"
                    /db_xref="taxon:10090"
                    /clone="8644.24"
                    /sex="male"
                    /cell_type="Embryonic stem cell"
                    /cell_line="E14"
                    /clone_lib="TIGEM gene trap library"
                    /note="Vector: pFLIP1"
ORIGIN

  Query Match             73.3%;  Score 11;  DB 9;  Length 46;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+05;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CTCCATTGATG 14
```

```
                  ||||||||||
Db          26 CTCCATTGATG 36


RESULT 10
BX659267/c
LOCUS       BX659267                 49 bp    DNA     linear   GSS 04-APR-2004
DEFINITION  Arabidopsis thaliana T-DNA flanking sequence GK-644G02-022818,
            genomic survey sequence.
ACCESSION   BX659267
VERSION     BX659267.1  GI:37615655
KEYWORDS    GSS.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Li,Y., Rosso,M.G., Strizhov,N., Viehoever,P. and Weisshaar,B.
  TITLE     GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for
            the identification of T-DNA insertion mutants in Arabidopsis
            thaliana
  JOURNAL   Bioinformatics 19 (11), 1441-1442 (2003)
  MEDLINE   22755829
   PUBMED   12874060
REFERENCE   2
  AUTHORS   Rosso,M.G., Li,Y., Strizhov,N., Reiss,B., Dekker,K. and
            Weisshaar,B.
  TITLE     An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
            flanking sequence tag-based reverse genetics
  JOURNAL   Plant Mol. Biol. 53 (1-2), 247-259 (2003)
  MEDLINE   23117147
   PUBMED   14756321
REFERENCE   3
  AUTHORS   Strizhov,N., Li,Y., Rosso,M.G., Viehoever,P., Dekker,K.A. and
            Weisshaar,B.
  TITLE     High-throughput generation of sequence indexes from T-DNA
            mutagenized Arabidopsis thaliana lines
  JOURNAL   BioTechniques 35 (6), 1164-1168 (2003)
   PUBMED   14682050
REFERENCE   4  (bases 1 to 49)
  AUTHORS   Strizhov,N., Rosso,M.G., Li,Y. and Weisshaar,B.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer
            Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
COMMENT     This sequence has been recovered from the left border of the T-DNA.
            It indicates an insertion close to or within gene At1g72180.
            Details on the protocols used for generation of the sequence are
            described in References 1-3. The sequences are generated at the MPI
            for Plant Breeding Research in the context of the GABI-Kat project.
            GABI-Kat is part of the German Plant Genomics program designated
            'GABI'. Information on line availability can be found at:
            http://www.mpiz-koeln.mpg.de/GABI-Kat/.
FEATURES             Location/Qualifiers
     source          1. .49
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /strain="Columbia 0"
                     /db_xref="taxon:3702"
                     /clone="GK-644G02-022818"
                     /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
                     /ecotype="Col-0"
                     /note="PCR was performed on DNA from Arabidopsis thaliana
                     plants (T1) which were transformed with the T-DNA from
                     vector pAC161 (GenBank accession number: AJ537514). The
                     lines contain one or more T-DNA insertions. The DNA
                     fragment(s) resulting from the PCR were directly sequenced
                     to determine the genomic sequence flanking the insertion.
                     T-DNA derived sequences were removed."
ORIGIN

  Query Match             73.3%;  Score 11;  DB 9;  Length 49;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+05;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CTCCATTGATG 14
              ||||||||||
Db         44 CTCCATTGATG 34


RESULT 11
AZ769902
LOCUS       AZ769902                 26 bp    DNA     linear   GSS 16-FEB-2001
DEFINITION  1M0571G06F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0571G06 F, genomic survey sequence.
ACCESSION   AZ769902
VERSION     AZ769902.1  GI:12890529
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0571  row: G  column: 06
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 26.
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0571G06"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

  Query Match             72.0%;  Score 10.8;  DB 8;  Length 26;
  Best Local Similarity   85.7%;  Pred. No. 1.7e+05;
```

```
  Matches   12;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATG 14
              ||||||| |||| |
Db         12 GTGCTCCCTTGACG 25


RESULT 12
AU256788/c
LOCUS       AU256788                 28 bp    mRNA    linear   EST 25-APR-2002
DEFINITION  AU256788 3'-directed mouse cDNA library Mus musculus cDNA clone
            BED0008978 3', mRNA sequence.
ACCESSION   AU256788
VERSION     AU256788.1  GI:20320779
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Kato,K. and Matoba,R.
  TITLE     Generation of expressed sequence tags from mouse brain
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Kikuya Kato
            Graduate School of Biological Sciences
            Nara Institute of Science and Technology
            8916-5 Takayama, Ikoma, Nara 630-0101, Japan
            Tel: 81-743-72-5581
            Fax: 81-743-72-5589
            Email: kkato@bs.aist-nara.ac.jp,
            URL:http://love2.aist-nara.ac.jp/BED/index.html.
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
                     /clone="BED0008978"
                     /tissue_type="brain"
                     /clone_lib="3'-directed mouse cDNA library"
ORIGIN

  Query Match             72.0%;  Score 10.8;  DB 1;  Length 28;
  Best Local Similarity   85.7%;  Pred. No. 1.7e+05;
  Matches   12;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TGCTCCATTGATGC 15
              | |||||||||| ||
Db         19 TCCTCCATTGAAGC 6


RESULT 13
AZ780454/c
LOCUS       AZ780454                 28 bp    DNA     linear   GSS 16-FEB-2001
DEFINITION  2M0017O16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0017O16 R, genomic survey sequence.
ACCESSION   AZ780454
VERSION     AZ780454.1  GI:12912132
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0017  row: O  column: 16
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 28.
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0017O16"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

  Query Match             72.0%;  Score 10.8;  DB 8;  Length 28;
  Best Local Similarity   85.7%;  Pred. No. 1.7e+05;
  Matches   12;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATG 14
              |||||||| | |||
Db         23 GTGCTCCAGTTATG 10


RESULT 14
TA59H06P/c
LOCUS       TA59H06P                 42 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  T. brucei sheared genomic DNA clone 59h06, forward sequence,
            genomic survey sequence.
ACCESSION   AL455680
VERSION     AL455680.1  GI:11857958
KEYWORDS    GSS.
SOURCE      Trypanosoma brucei
  ORGANISM  Trypanosoma brucei
            Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE   1  (bases 1 to 42)
  AUTHORS   Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
            Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
            Melville,S.E., Rajandream,M.A. and Barrell,B.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
            project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
            Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
            nh1@sanger.ac.uk
COMMENT     Constructed at the Institute for Genomic Research (TIGR),
            Rockville, MD. Genomic DNA isolated from a cloned population of
```

Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES Location/Qualifiers
source 1. .42
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="59h06"

ORIGIN

Query Match 72.0%; Score 10.8; DB 9; Length 42;
Best Local Similarity 85.7%; Pred. No. 1.8e+05;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy          1 GTGCTCCATTGATG 14
              |||| ||||||| |
Db         22 GTGCCCCATTGAAG 9
```

RESULT 15
CV521218
LOCUS CV521218 43 bp mRNA linear EST 06-OCT-2004
DEFINITION 0089P0056Z.x0_D02 Mimulus guttatus library 2 Mimulus guttatus cDNA clone 0089P0056Z.x0_D02, mRNA sequence.
ACCESSION CV521218
VERSION CV521218.1 GI:53847750
KEYWORDS EST.
SOURCE Mimulus guttatus (spotted monkey flower)
ORGANISM Mimulus guttatus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiids; Lamiales; Lamiales incertae sedis; Mimuleae; Mimulus.
REFERENCE 1 (bases 1 to 43)
AUTHORS Willis,J., Vision,T., Dietrich,F.S. and Allen,A.
TITLE Mimulus guttatus cDNA sequence
JOURNAL Unpublished (2004)
COMMENT Contact: Willis J
Department of Biology
Duke University
072-A Biological Sciences Science Drive, Durham, NC 27708, USA
Tel: 919 660 7340
Fax: 919 660 7293
Email: jwillis@duke.edu
Plate: 0089P0056 row: 02 column: D
Seq primer: T7
High quality sequence start: 80
High quality sequence stop: 132.

FEATURES Location/Qualifiers
source 1. .43
/organism="Mimulus guttatus"
/mol_type="mRNA"
/db_xref="taxon:4155"
/clone="0089P0056Z.x0_D02"
/clone_lib="Mimulus guttatus library 2"
/note="Vector: pGEM-T Easy; a Mimulus guttatus cDNA library"

ORIGIN

Query Match 72.0%; Score 10.8; DB 7; Length 43;
Best Local Similarity 85.7%; Pred. No. 1.8e+05;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy          1 GTGCTCCATTGATG 14
                ||| || |||||||
Db         30 GTGTTCGATTGATG 43
```

Search completed: June 21, 2005, 06:51:11
Job time : 3008 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: June 21, 2005, 01:08:35 ; Search time 3103 Seconds
(without alignments)
184.004 Million cell updates/sec

Title: US-10-075-994A-1
Perfect score: 15
Sequence: 1 gtgctccattgatgc 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	15	100.0	165	9	CG531606	CG531606 OST114549
c 2	15	100.0	166	9	CG497924	CG497924 OST38825
c 3	15	100.0	207	1	AA306005	AA306005 EST177032
c 4	15	100.0	229	9	CG605299	CG605299 OST281834
c 5	15	100.0	231	9	CG661765	CG661765 OST443394
c 6	15	100.0	253	9	CG580338	CG580338 OST219649
7	15	100.0	274	2	BF897689	BF897689 QV1-MT022
c 8	15	100.0	276	9	CG664359	CG664359 OST451337
c 9	15	100.0	282	9	CG546546	CG546546 OST146106
c 10	15	100.0	293	2	BF468476	BF468476 UI-M-CD0-
c 11	15	100.0	294	1	AA332421	AA332421 EST36381
c 12	15	100.0	300	9	CG577036	CG577036 OST212398
c 13	15	100.0	300	9	CG591346	CG591346 OST245811
c 14	15	100.0	308	9	CG513061	CG513061 OST66238
c 15	15	100.0	309	7	CN295726	CN295726 170005321
16	15	100.0	327	7	D43526	D43526 D43526 Rice
c 17	15	100.0	328	5	BY329807	BY329807 BY329807
c 18	15	100.0	335	5	BY324333	BY324333 BY324333
c 19	15	100.0	340	5	BY068929	BY068929 BY068929
20	15	100.0	346	5	BQ375054	BQ375054 MR4-TN011
c 21	15	100.0	349	5	BY063442	BY063442 BY063442
c 22	15	100.0	351	9	CG633156	CG633156 OST352509
c 23	15	100.0	353	6	CB779923	CB779923 AMGNNUC:N
c 24	15	100.0	355	5	BY147345	BY147345 BY147345
c 25	15	100.0	355	9	CG623442	CG623442 OST325479
c 26	15	100.0	358	5	BY014540	BY014540 BY014540
c 27	15	100.0	359	5	BY304066	BY304066 BY304066
c 28	15	100.0	362	5	BY036035	BY036035 BY036035
c 29	15	100.0	362	9	CG555213	CG555213 OST169619
c 30	15	100.0	366	5	BY063180	BY063180 BY063180
c 31	15	100.0	366	5	BY318790	BY318790 BY318790
c 32	15	100.0	367	5	BY014670	BY014670 BY014670
c 33	15	100.0	374	5	BY071821	BY071821 BY071821
c 34	15	100.0	376	5	BY280317	BY280317 BY280317
c 35	15	100.0	379	2	BE244097	BE244097 TCBAP1E06
c 36	15	100.0	379	5	BY047534	BY047534 BY047534
c 37	15	100.0	382	1	AU077313	AU077313 AU077313
c 38	15	100.0	384	5	BY087978	BY087978 BY087978
c 39	15	100.0	387	1	AA017736	AA017736 mh41b05.r
c 40	15	100.0	388	9	CG603416	CG603416 OST278044
c 41	15	100.0	391	5	BY061467	BY061467 BY061467
c 42	15	100.0	399	5	BY279803	BY279803 BY279803
c 43	15	100.0	400	5	BY288082	BY288082 BY288082
c 44	15	100.0	401	6	CB698634	CB698634 AMGNNUC:M
c 45	15	100.0	406	5	BY314742	BY314742 BY314742

ALIGNMENTS

RESULT 1
CG531606/c
LOCUS CG531606 165 bp mRNA linear GSS 01-OCT-2003
DEFINITION OST114549 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST114549, mRNA sequence.
ACCESSION CG531606
VERSION CG531606.1 GI:37318178
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 165)
AUTHORS Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J., Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A., Friddle,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C., Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D., Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z., Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N., Zhu,Q., Person,C. and Sands,A.T.
TITLE Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
COMMENT Contact: Zambrowicz BP
OmniBank
Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
Class: Gene Trap.
FEATURES Location/Qualifiers
source 1. .165
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129Sv/Ev"
/db_xref="taxon:10090"
/clone="OST114549"
/cell_type="embryonic stem cell"
/clone_lib="Mus musculus 129Sv/Ev"
ORIGIN

Query Match 100.0%; Score 15; DB 9; Length 165;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCTCCATTGATGC 15

```
              ||||||||||||||||
Db         39 GTGCTCCATTGATGC 25


RESULT 2
CG497924/c
LOCUS       CG497924                166 bp    mRNA    linear   GSS 01-OCT-2003
DEFINITION  OST38825 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST38825,
            mRNA sequence.
ACCESSION   CG497924
VERSION     CG497924.1  GI:37267955
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 166)
  AUTHORS   Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
            Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,
            Friddle,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,
            Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,
            Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
            Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,
            Zhu,Q., Person,C. and Sands,A.T.
  TITLE     Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
            screen to identify potential targets for therapeutic intervention
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
COMMENT     Contact: Zambrowicz BP
            OmniBank
            Lexicon Genetics Incorporated
            4000 Research Forest Drive, The Woodlands, TX 77381, USA
            Email: materials@lexgen.com
            Gene trap sequence tag generated by 3' RACE from mouse ES cells as
            described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
            Class: Gene Trap.
FEATURES             Location/Qualifiers
     source          1. .166
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="129Sv/Ev"
                     /db_xref="taxon:10090"
                     /clone="OST38825"
                     /cell_type="embryonic stem cell"
                     /clone_lib="Mus musculus 129Sv/Ev"
ORIGIN

  Query Match             100.0%;  Score 15;  DB 9;  Length 166;
  Best Local Similarity   100.0%;  Pred. No. 7.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATGC 15
              ||||||||||||||||
Db         35 GTGCTCCATTGATGC 21


RESULT 3
AA306005/c
LOCUS       AA306005                207 bp    mRNA    linear   EST 18-APR-1997
DEFINITION  EST177032 Jurkat T-cells VI Homo sapiens cDNA 5' end similar to
            proto-oncogene raf, mRNA sequence.
ACCESSION   AA306005
VERSION     AA306005.1  GI:1958375
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 207)
  AUTHORS   Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
            Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
            White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
            Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
            Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
            Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr.,
            Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
            Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
            Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
            Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
            Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
            Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
            He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
            Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.,
            Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M.,
            Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
            Fraser,C.M. and Venter,J.C.
  TITLE     Initial assessment of human gene diversity and expression patterns
            based upon 83 million nucleotides of cDNA sequence
  JOURNAL   Nature 377 (6547 Suppl), 3-174 (1995)
  MEDLINE   96026280
   PUBMED   7566098
COMMENT     Other_ESTs: THC192945
            Contact: Kerlavage, AR
            Bioinformatics
            The Institute for Genomic Research
            9712 Medical Center Drive, Rockville, MD 20850 USA
            Tel: 3018699056
            Fax: 3018699423
            Email: arkerlav@tigr.org
            For clone availability, additional sequence and expression
            information related to this EST, please check the TIGR Human Gene
            Index (http://www.tigr.org/tdb/hgi/hgi.html)
            Seq primer: M13 Reverse.
FEATURES             Location/Qualifiers
     source          1. .207
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="ATCC (inhost):160136"
                     /db_xref="taxon:9606"
                     /cell_type="T-lymphocyte"
                     /clone_lib="Jurkat T-cells VI"
                     /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                     XhoI"
ORIGIN

  Query Match             100.0%;  Score 15;  DB 1;  Length 207;
  Best Local Similarity   100.0%;  Pred. No. 7.6e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATGC 15
              ||||||||||||||||
Db         40 GTGCTCCATTGATGC 26


RESULT 4
CG605299/c
LOCUS       CG605299                229 bp    mRNA    linear   GSS 02-OCT-2003
DEFINITION  OST281834 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST281834,
            mRNA sequence.
ACCESSION   CG605299
VERSION     CG605299.1  GI:37427977
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 229)
  AUTHORS   Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
            Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,
            Friddle,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,
            Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,
            Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
            Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,
            Zhu,Q., Person,C. and Sands,A.T.
  TITLE     Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
            screen to identify potential targets for therapeutic intervention
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
```

```
COMMENT     Contact: Zambrowicz BP
            OmniBank
            Lexicon Genetics Incorporated
            4000 Research Forest Drive, The Woodlands, TX 77381, USA
            Email: materials@lexgen.com
            Gene trap sequence tag generated by 3' RACE from mouse ES cells as
            described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
            Class: Gene Trap.
FEATURES             Location/Qualifiers
     source          1. .229
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="129Sv/Ev"
                     /db_xref="taxon:10090"
                     /clone="OST281834"
                     /cell_type="embryonic stem cell"
                     /clone_lib="Mus musculus 129Sv/Ev"
ORIGIN

  Query Match             100.0%;  Score 15;  DB 9;  Length 229;
  Best Local Similarity   100.0%;  Pred. No. 7.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATGC 15
              |||||||||||||||
Db         43 GTGCTCCATTGATGC 29


RESULT 5
CG661765/c
LOCUS       CG661765                231 bp    mRNA    linear   GSS 02-OCT-2003
DEFINITION  OST443394 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST443394,
            mRNA sequence.
ACCESSION   CG661765
VERSION     CG661765.1  GI:37485614
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 231)
  AUTHORS   Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
            Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,
            Friddle,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,
            Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,
            Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
            Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,
            Zhu,Q., Person,C. and Sands,A.T.
  TITLE     Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
            screen to identify potential targets for therapeutic intervention
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
COMMENT     Contact: Zambrowicz BP
            OmniBank
            Lexicon Genetics Incorporated
            4000 Research Forest Drive, The Woodlands, TX 77381, USA
            Email: materials@lexgen.com
            Gene trap sequence tag generated by 3' RACE from mouse ES cells as
            described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
            Class: Gene Trap.
FEATURES             Location/Qualifiers
     source          1. .231
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="129Sv/Ev"
                     /db_xref="taxon:10090"
                     /clone="OST443394"
                     /cell_type="embryonic stem cell"
                     /clone_lib="Mus musculus 129Sv/Ev"
ORIGIN

  Query Match             100.0%;  Score 15;  DB 9;  Length 231;
  Best Local Similarity   100.0%;  Pred. No. 7.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATGC 15
              |||||||||||||||
Db         30 GTGCTCCATTGATGC 16


RESULT 6
CG580338/c
LOCUS       CG580338                253 bp    mRNA    linear   GSS 02-OCT-2003
DEFINITION  OST219649 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST219649,
            mRNA sequence.
ACCESSION   CG580338
VERSION     CG580338.1  GI:37375289
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 253)
  AUTHORS   Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
            Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,
            Friddle,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,
            Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,
            Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
            Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,
            Zhu,Q., Person,C. and Sands,A.T.
  TITLE     Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
            screen to identify potential targets for therapeutic intervention
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
COMMENT     Contact: Zambrowicz BP
            OmniBank
            Lexicon Genetics Incorporated
            4000 Research Forest Drive, The Woodlands, TX 77381, USA
            Email: materials@lexgen.com
            Gene trap sequence tag generated by 3' RACE from mouse ES cells as
            described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
            Class: Gene Trap.
FEATURES             Location/Qualifiers
     source          1. .253
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="129Sv/Ev"
                     /db_xref="taxon:10090"
                     /clone="OST219649"
                     /cell_type="embryonic stem cell"
                     /clone_lib="Mus musculus 129Sv/Ev"
ORIGIN

  Query Match             100.0%;  Score 15;  DB 9;  Length 253;
  Best Local Similarity   100.0%;  Pred. No. 7.9e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATGC 15
              |||||||||||||||
Db         42 GTGCTCCATTGATGC 28


RESULT 7
BF897689
LOCUS       BF897689                274 bp    mRNA    linear   EST 18-JAN-2001
DEFINITION  QV1-MT0224-281100-512-b01 MT0224 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BF897689
VERSION     BF897689.1  GI:12289148
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 274)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
```

```
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
   PUBMED   10737800
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=QV1&t2=QV1-MT0224-
            281100-512-b01&t3=2000-11-28&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 27
            High quality sequence stop: 274.
FEATURES             Location/Qualifiers
     source          1. .274
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /dev_stage="Adult"
                     /clone_lib="MT0224"
                     /note="Organ: marrow; Vector: puc18; Site_1: SmaI; Site_2:
                     SmaI; A mini-library was made by cloning products derived
                     from  ORESTES PCR (U.S. Letters Patent application No.
                     196,716 -  Ludwig Institute for Cancer Research) profiles
                     into  the pUC 18 vector. Reverse transcription of tissue
                     mRNA and cDNA amplification were performed under low
                     stringency conditions."
ORIGIN

  Query Match             100.0%;  Score 15;  DB 2;  Length 274;
  Best Local Similarity   100.0%;  Pred. No. 8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATGC 15
              |||||||||||||||
Db        170 GTGCTCCATTGATGC 184


RESULT 8
CG664359/c
LOCUS       CG664359                276 bp    mRNA    linear   GSS 02-OCT-2003
DEFINITION  OST451337 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST451337,
            mRNA sequence.
ACCESSION   CG664359
VERSION     CG664359.1  GI:37488208
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 276)
  AUTHORS   Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
            Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,
            Friddle,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,
            Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,
            Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
            Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,
            Zhu,Q., Person,C. and Sands,A.T.
  TITLE     Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
            screen to identify potential targets for therapeutic intervention
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
COMMENT     Contact: Zambrowicz BP
            OmniBank
            Lexicon Genetics Incorporated
            4000 Research Forest Drive, The Woodlands, TX 77381, USA
            Email: materials@lexgen.com
            Gene trap sequence tag generated by 3' RACE from mouse ES cells as
            described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
            Class: Gene Trap.
FEATURES             Location/Qualifiers
     source          1. .276
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="129Sv/Ev"
                     /db_xref="taxon:10090"
                     /clone="OST451337"
                     /cell_type="embryonic stem cell"
                     /clone_lib="Mus musculus 129Sv/Ev"
ORIGIN

  Query Match             100.0%;  Score 15;  DB 9;  Length 276;
  Best Local Similarity   100.0%;  Pred. No. 8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATGC 15
              |||||||||||||||
Db         38 GTGCTCCATTGATGC 24


RESULT 9
CG546546/c
LOCUS       CG546546                282 bp    mRNA    linear   GSS 01-OCT-2003
DEFINITION  OST146106 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST146106,
            mRNA sequence.
ACCESSION   CG546546
VERSION     CG546546.1  GI:37333133
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 282)
  AUTHORS   Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
            Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,
            Friddle,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,
            Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,
            Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
            Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,
            Zhu,Q., Person,C. and Sands,A.T.
  TITLE     Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
            screen to identify potential targets for therapeutic intervention
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
COMMENT     Contact: Zambrowicz BP
            OmniBank
            Lexicon Genetics Incorporated
            4000 Research Forest Drive, The Woodlands, TX 77381, USA
            Email: materials@lexgen.com
            Gene trap sequence tag generated by 3' RACE from mouse ES cells as
            described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
            Class: Gene Trap.
FEATURES             Location/Qualifiers
     source          1. .282
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="129Sv/Ev"
                     /db_xref="taxon:10090"
                     /clone="OST146106"
                     /cell_type="embryonic stem cell"
                     /clone_lib="Mus musculus 129Sv/Ev"
ORIGIN

  Query Match             100.0%;  Score 15;  DB 9;  Length 282;
  Best Local Similarity   100.0%;  Pred. No. 8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATGC 15
              |||||||||||||||
```

```
Db         43 GTGCTCCATTGATGC 29


RESULT 10
BF468476/c
LOCUS       BF468476                293 bp    mRNA    linear   EST 04-DEC-2000
DEFINITION  UI-M-CD0-ayj-e-12-0-UI.r1 NIH_BMAP_Ret2 Mus musculus cDNA clone
            UI-M-CD0-ayj-e-12-0-UI 5', mRNA sequence.
ACCESSION   BF468476
VERSION     BF468476.1  GI:11537659
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 293)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
   PUBMED   8889548
COMMENT     Contact: Chin, H
            National Institute of Mental Health
            6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
            20892-9643, USA
            Tel: 301 443 1706
            Fax: 301 443 9890
            Email: mEST@mail.nih.gov
            cDNA Library Preparation: M.B. Soares Lab Clone distribution:
            Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It
            should be noted that Bento Soares is generating a small number of
            additional specialized non-redundant arrays of BMAP cDNAs whose
            availability will be considered under appropriate and limited
            collaborative arrangements The following repetitive elements were
            found in this cDNA sequence: 60-91, >GC_rich#Low_complexity
            Seq primer: M13 Reverse.
FEATURES             Location/Qualifiers
     source          1. .293
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UI-M-CD0-ayj-e-12-0-UI"
                     /dev_stage="1 day"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="NIH_BMAP_Ret2"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; The
                     NIH_BMAP_Ret2 library is derived from mouse neonatal
                     retina tissue. For a detailed description of the library
                     from which this clone was derived, please visit our web
                     site at brainest.eng.uiowa.edu. The tissue for this
                     library was contributed by Dr. Xin-Yuan Fu, Yale
                     University School of Medicine"
ORIGIN

  Query Match           100.0%;  Score 15;  DB 2;  Length 293;
  Best Local Similarity  100.0%;  Pred. No. 8.1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATGC 15
              |||||||||||||||
Db        218 GTGCTCCATTGATGC 204


RESULT 11
AA332421/c
LOCUS       AA332421                294 bp    mRNA    linear   EST 21-APR-1997
DEFINITION  EST36381 Embryo, 8 week I Homo sapiens cDNA 5' end similar to
            proto-oncogene raf, mRNA sequence.
ACCESSION   AA332421
VERSION     AA332421.1  GI:1984686
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 294)
  AUTHORS   Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
            Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
            White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
            Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
            Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
            Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr.,
            Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
            Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
            Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
            Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
            Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
            Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
            He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
            Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.,
            Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M.,
            Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
            Fraser,C.M. and Venter,J.C.
  TITLE     Initial assessment of human gene diversity and expression patterns
            based upon 83 million nucleotides of cDNA sequence
  JOURNAL   Nature 377 (6547 Suppl), 3-174 (1995)
  MEDLINE   96026280
   PUBMED   7566098
COMMENT     Other_ESTs: THC192945
            Contact: Kerlavage, AR
            Bioinformatics
            The Institute for Genomic Research
            9712 Medical Center Drive, Rockville, MD 20850 USA
            Tel: 3018699056
            Fax: 3018699423
            Email: arkerlav@tigr.org
            For clone availability, additional sequence and expression
            information related to this EST, please check the TIGR Human Gene
            Index (http://www.tigr.org/tdb/hgi/hgi.html)
            Seq primer: M13 Reverse.
FEATURES             Location/Qualifiers
     source          1. .294
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="ATCC (inhost):134082"
                     /db_xref="taxon:9606"
                     /dev_stage="embryo, 8 wks"
                     /clone_lib="Embryo, 8 week I"
                     /note="Organ: Embryo, 8 weeks; Vector: pBluescript SK-;
                     Site_1: EcoRI; Site_2: XhoI"
ORIGIN

  Query Match           100.0%;  Score 15;  DB 1;  Length 294;
  Best Local Similarity  100.0%;  Pred. No. 8.1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATGC 15
              |||||||||||||||
Db         40 GTGCTCCATTGATGC 26


RESULT 12
CG577036/c
LOCUS       CG577036                300 bp    mRNA    linear   GSS 02-OCT-2003
DEFINITION  OST212398 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST212398,
            mRNA sequence.
ACCESSION   CG577036
VERSION     CG577036.1  GI:37367640
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
```

```
REFERENCE   1  (bases 1 to 300)
  AUTHORS   Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
            Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,
            Friddle,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,
            Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,
            Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
            Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,
            Zhu,Q., Person,C. and Sands,A.T.
  TITLE     Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
            screen to identify potential targets for therapeutic intervention
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
COMMENT     Contact: Zambrowicz BP
            OmniBank
            Lexicon Genetics Incorporated
            4000 Research Forest Drive, The Woodlands, TX 77381, USA
            Email: materials@lexgen.com
            Gene trap sequence tag generated by 3' RACE from mouse ES cells as
            described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
            Class: Gene Trap.
FEATURES             Location/Qualifiers
     source          1. .300
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="129Sv/Ev"
                     /db_xref="taxon:10090"
                     /clone="OST212398"
                     /cell_type="embryonic stem cell"
                     /clone_lib="Mus musculus 129Sv/Ev"
ORIGIN

  Query Match             100.0%;  Score 15;  DB 9;  Length 300;
  Best Local Similarity   100.0%;  Pred. No. 8.1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATGC 15
              ||||||||||||||||
Db         42 GTGCTCCATTGATGC 28


RESULT 13
CG591346/c
LOCUS       CG591346                300 bp    mRNA    linear   GSS 02-OCT-2003
DEFINITION  OST245811 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST245811,
            mRNA sequence.
ACCESSION   CG591346
VERSION     CG591346.1  GI:37399162
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 300)
  AUTHORS   Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
            Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,
            Friddle,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,
            Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,
            Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
            Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,
            Zhu,Q., Person,C. and Sands,A.T.
  TITLE     Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
            screen to identify potential targets for therapeutic intervention
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
COMMENT     Contact: Zambrowicz BP
            OmniBank
            Lexicon Genetics Incorporated
            4000 Research Forest Drive, The Woodlands, TX 77381, USA
            Email: materials@lexgen.com
            Gene trap sequence tag generated by 3' RACE from mouse ES cells as
            described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
            Class: Gene Trap.
FEATURES             Location/Qualifiers
     source          1. .300
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="129Sv/Ev"
                     /db_xref="taxon:10090"
                     /clone="OST245811"
                     /cell_type="embryonic stem cell"
                     /clone_lib="Mus musculus 129Sv/Ev"
ORIGIN

  Query Match             100.0%;  Score 15;  DB 9;  Length 300;
  Best Local Similarity   100.0%;  Pred. No. 8.1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATGC 15
              ||||||||||||||||
Db         41 GTGCTCCATTGATGC 27


RESULT 14
CG513061/c
LOCUS       CG513061                308 bp    mRNA    linear   GSS 01-OCT-2003
DEFINITION  OST66238 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST66238,
            mRNA sequence.
ACCESSION   CG513061
VERSION     CG513061.1  GI:37299634
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 308)
  AUTHORS   Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
            Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,
            Friddle,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,
            Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,
            Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
            Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,
            Zhu,Q., Person,C. and Sands,A.T.
  TITLE     Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
            screen to identify potential targets for therapeutic intervention
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
COMMENT     Contact: Zambrowicz BP
            OmniBank
            Lexicon Genetics Incorporated
            4000 Research Forest Drive, The Woodlands, TX 77381, USA
            Email: materials@lexgen.com
            Gene trap sequence tag generated by 3' RACE from mouse ES cells as
            described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
            Class: Gene Trap.
FEATURES             Location/Qualifiers
     source          1. .308
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="129Sv/Ev"
                     /db_xref="taxon:10090"
                     /clone="OST66238"
                     /cell_type="embryonic stem cell"
                     /clone_lib="Mus musculus 129Sv/Ev"
ORIGIN

  Query Match             100.0%;  Score 15;  DB 9;  Length 308;
  Best Local Similarity   100.0%;  Pred. No. 8.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATGC 15
              ||||||||||||||||
Db         40 GTGCTCCATTGATGC 26


RESULT 15
CN295726/c
LOCUS       CN295726                309 bp    mRNA    linear   EST 16-MAY-2004
DEFINITION  17000532192143 GRN_ES Homo sapiens cDNA 5', mRNA sequence.
ACCESSION   CN295726
```

```
VERSION     CN295726.1  GI:47312140
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 309)
  AUTHORS   Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,
            Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R.,
            Lebkowski,J and Stanton,L.W.
  TITLE     Transcriptome characterization elucidates signaling networks that
            control human ES cell growth and differentiation
  JOURNAL   Nat. Biotechnol. 22 (6), 707-716 (2004)
COMMENT     Contact: Brandenberger R
            Regenerative Medicine
            Geron Corporation
            230 Constitution Drive, Menlo Park, CA 94025, USA
            Tel: 650 473 8658
            Fax: 650 473 7760
            Email: rbrandenberger@geron.com
            Insert Length: 309   Std Error: 0.00.
FEATURES             Location/Qualifiers
     source          1. .309
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /tissue_type="embryonic stem cells, cell lines H1, H7, and
                     H9"
                     /clone_lib="GRN_ES"
                     /note="oligo dT primed, full-length enriched cDNA library
                     from undifferentiated hES cell lines H1 (p32), H7 (p29),
                     and H9 (p26) maintained in feeder-free conditions"
ORIGIN

  Query Match             100.0%;  Score 15;  DB 7;  Length 309;
  Best Local Similarity   100.0%;  Pred. No. 8.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATGC 15
              |||||||||||||||
Db        278 GTGCTCCATTGATGC 264


Search completed: June 21, 2005, 03:49:24
Job time : 3110 secs
```

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: June 20, 2005, 20:52:15 ; Search time 1678 Seconds
(without alignments)
433.152 Million cell updates/sec

Title: US-10-075-994A-1
Perfect score: 15
Sequence: 1 gtgctccattgatgc 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		15	100.0	15	6	AR110775	AR110775 Sequence
2	c	15	100.0	15	6	AR110777	AR110777 Sequence
3		15	100.0	15	6	AR167449	AR167449 Sequence
4		15	100.0	15	6	CQ789712	CQ789712 Sequence
5		15	100.0	15	6	AR310685	AR310685 Sequence
6	c	15	100.0	15	6	AR310687	AR310687 Sequence
7		15	100.0	15	6	AX797662	AX797662 Sequence
8		15	100.0	15	6	AX957646	AX957646 Sequence
9		15	100.0	15	6	AX957740	AX957740 Sequence
10		15	100.0	15	6	AX958145	AX958145 Sequence
11		15	100.0	15	6	BD106498	BD106498 High effi
12		15	100.0	20	6	AR073978	AR073978 Sequence
13		15	100.0	20	6	AR216002	AR216002 Sequence
14		15	100.0	25	6	AR110776	AR110776 Sequence
15		15	100.0	25	6	AR310686	AR310686 Sequence
16	c	15	100.0	487	10	AB077145	AB077145 Mus muscu
17		15	100.0	1496	8	AK064133	AK064133 Oryza sat
18	c	15	100.0	2524	10	RATRAFA	M15427 Rat c-raf p
19	c	15	100.0	2811	10	AB057663	AB057663 Mus muscu
20	c	15	100.0	2935	10	BC015273	BC015273 Mus muscu
21	c	15	100.0	2970	10	BC062071	BC062071 Rattus no
22	c	15	100.0	2975	6	AR473559	AR473559 Sequence
23	c	15	100.0	2977	6	AR073995	AR073995 Sequence
24	c	15	100.0	2977	6	AR110473	AR110473 Sequence
25	c	15	100.0	2977	6	BD237320	BD237320 Modulatio
26	c	15	100.0	2977	6	I34402	I34402 Sequence 1
27	c	15	100.0	2977	6	I96180	I96180 Sequence 17
28	c	15	100.0	2977	6	AR215978	AR215978 Sequence
29	c	15	100.0	2977	6	AR337749	AR337749 Sequence
30	c	15	100.0	2977	6	AR360020	AR360020 Sequence
31	c	15	100.0	2977	6	AX022819	AX022819 Sequence
32	c	15	100.0	2977	6	AX030539	AX030539 Sequence
33	c	15	100.0	2977	6	AX337827	AX337827 Sequence
34	c	15	100.0	2977	6	AX622838	AX622838 Sequence
35	c	15	100.0	2977	6	AX696362	AX696362 Sequence
36	c	15	100.0	2977	6	AX777762	AX777762 Sequence
37	c	15	100.0	2977	6	BD091455	BD091455 Transgeni
38	c	15	100.0	2977	9	HSRAFR	X03484 Human mRNA
39	c	15	100.0	2981	6	CQ723686	CQ723686 Sequence
40	c	15	100.0	3216	9	BC018119	BC018119 Homo sapi
41	c	15	100.0	66275	2	AC100586	AC100586 Mus muscu
42		15	100.0	71328	2	AC025497	AC025497 Homo sapi
43	c	15	100.0	82374	9	AY271661	AY271661 Homo sapi
44		15	100.0	93614	9	AL139294	AL139294 Human DNA
45	c	15	100.0	112234	8	AP006147	AP006147 Lotus cor

ALIGNMENTS

RESULT 1
AR110775
LOCUS AR110775 15 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 1 from patent US 6126965.
ACCESSION AR110775
VERSION AR110775.1 GI:12827623
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Kasid,U., Gokhale,P., Dritschilo,A. and Rahman,A.
TITLE Liposomes containing oligonucleotides
JOURNAL Patent: US 6126965-A 1 03-OCT-2000;
FEATURES Location/Qualifiers
source 1. .15
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN

Query Match 100.0%; Score 15; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCTCCATTGATGC 15
||||||||||||||||
Db 1 GTGCTCCATTGATGC 15

RESULT 2
AR110777/c
LOCUS AR110777 15 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 3 from patent US 6126965.
ACCESSION AR110777
VERSION AR110777.1 GI:12827625
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Kasid,U., Gokhale,P., Dritschilo,A. and Rahman,A.
TITLE Liposomes containing oligonucleotides

```
  JOURNAL   Patent: US 6126965-A 3 03-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match           100.0%;  Score 15;  DB 6;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATGC 15
              |||||||||||||||
Db         15 GTGCTCCATTGATGC 1


RESULT 3
AR167449
LOCUS       AR167449                 15 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 15 from patent US 6287591.
ACCESSION   AR167449
VERSION     AR167449.1  GI:17903229
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Semple,S.C., Klimuk,S.K., Harasym,T., Hope,M.J., Ansell,S.M.,
            Cullis,P., Scherrer,P. and Debeyer,D.
  TITLE     Charged therapeutic agents encapsulated in lipid particles
            containing four lipid components
  JOURNAL   Patent: US 6287591-A 15 11-SEP-2001;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match           100.0%;  Score 15;  DB 6;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATGC 15
              |||||||||||||||
Db          1 GTGCTCCATTGATGC 15


RESULT 4
CQ789712
LOCUS       CQ789712                 15 bp    DNA     linear   PAT 29-MAR-2004
DEFINITION  Sequence 1 from Patent WO2004017944.
ACCESSION   CQ789712
VERSION     CQ789712.1  GI:45823264
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Zhang,J.A. and Ahmad,I.
  TITLE     Liposomal gemcitabine compositions for better drug delivery
  JOURNAL   Patent: WO.2004017944-A 1 04-MAR-2004;
            Neopharm, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Anti-raf-oligonucleotides"
ORIGIN

  Query Match           100.0%;  Score 15;  DB 6;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATGC 15
              |||||||||||||||
Db          1 GTGCTCCATTGATGC 15


RESULT 5
AR310685
LOCUS       AR310685                 15 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 1 from patent US 6559129.
ACCESSION   AR310685
VERSION     AR310685.1  GI:31703829
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kasid,U., Gokhale,P., Zhang,C., Dritschilo,A. and Rahman,A.
  TITLE     Cationic liposomal delivery system and therapeutic use thereof
  JOURNAL   Patent: US 6559129-A 1 06-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match           100.0%;  Score 15;  DB 6;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATGC 15
              |||||||||||||||
Db          1 GTGCTCCATTGATGC 15


RESULT 6
AR310687/c
LOCUS       AR310687                 15 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 3 from patent US 6559129.
ACCESSION   AR310687
VERSION     AR310687.1  GI:31703831
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kasid,U., Gokhale,P., Zhang,C., Dritschilo,A. and Rahman,A.
  TITLE     Cationic liposomal delivery system and therapeutic use thereof
  JOURNAL   Patent: US 6559129-A 3 06-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match           100.0%;  Score 15;  DB 6;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATGC 15
              |||||||||||||||
Db         15 GTGCTCCATTGATGC 1


RESULT 7
AX797662
LOCUS       AX797662                 15 bp    DNA     linear   PAT 04-OCT-2003
DEFINITION  Sequence 25 from Patent WO03039595.
ACCESSION   AX797662
VERSION     AX797662.1  GI:37518090
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
```

```
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Semple,S., Klimuk,S. and Yuan,Z.N.
  TITLE     Mucosal adjuvants comprising an oligonucleotide and a cationic
            lipid
  JOURNAL   Patent: WO 03039595-A 25 15-MAY-2003;
            Inex Pharmaceuticals Corp. (CA)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             100.0%;  Score 15;  DB 6;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATGC 15
              |||||||||||||||
Db          1 GTGCTCCATTGATGC 15


RESULT 8
AX957646
LOCUS       AX957646                 15 bp    DNA     linear   PAT 08-JAN-2004
DEFINITION  Sequence 25 from Patent WO03094963.
ACCESSION   AX957646
VERSION     AX957646.1  GI:40785518
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Tam,Y.K., Semple,S., Klimuk,S. and Chikh,G.
  TITLE     Methylated immunostimulatory oligonucleotides and methods of using
            the same
  JOURNAL   Patent: WO 03094963-A 25 20-NOV-2003;
            Inex Pharmaceuticals Corporation (CA)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             100.0%;  Score 15;  DB 6;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATGC 15
              |||||||||||||||
Db          1 GTGCTCCATTGATGC 15


RESULT 9
AX957740
LOCUS       AX957740                 15 bp    DNA     linear   PAT 08-JAN-2004
DEFINITION  Sequence 25 from Patent WO03094828.
ACCESSION   AX957740
VERSION     AX957740.1  GI:40785558
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Tam,Y.K., Semple,S., Klimuk,S. and Chikh,G.
  TITLE     Cancer vaccines and methods of using the same
  JOURNAL   Patent: WO 03094828-A 25 20-NOV-2003;
            Inex Pharmaceuticals Corp. (CA)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             100.0%;  Score 15;  DB 6;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATGC 15
              |||||||||||||||
Db          1 GTGCTCCATTGATGC 15


RESULT 10
AX958145
LOCUS       AX958145                 15 bp    DNA     linear   PAT 08-JAN-2004
DEFINITION  Sequence 25 from Patent WO03094829.
ACCESSION   AX958145
VERSION     AX958145.1  GI:40785809
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Semple,S., Chikh,G., Hope,M.J. and Tam,Y.K.
  TITLE     Pathogen vaccines and methods for using the same
  JOURNAL   Patent: WO 03094829-A 25 20-NOV-2003;
            Inex Pharmaceuticals Corp. (CA)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             100.0%;  Score 15;  DB 6;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATGC 15
              |||||||||||||||
Db          1 GTGCTCCATTGATGC 15


RESULT 11
BD106498
LOCUS       BD106498                 15 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  High efficiency encapsulation of charged therapeutic agents in
            lipid vesicles.
ACCESSION   BD106498
VERSION     BD106498.1  GI:23201316
KEYWORDS    JP 2002501511-A/15.
SOURCE      Chlamydia sp.
  ORGANISM  Chlamydia sp.
            Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Semple,S.C., Klimuk,S.K., Harasym,T., Hope,M.J., Ansel,S.M.,
            Cullis,P., Scherrer,P. and Debeyer,D.S.
  TITLE     High efficiency encapsulation of charged therapeutic agents in
            lipid vesicles
  JOURNAL   Patent: JP 2002501511-A 15 15-JAN-2002;
            INEX PHARMACEUTICALS CORP
COMMENT     PN   JP 2002501511-A/15
            PD   15-JAN-2002
            PF   14-MAY-1998 JP 1998548646
            PI   SEAN C SEMPLE,SANDRA K KLIMUK,TROY HARASYM,MICHAEL J HOPE, PI
             STEVEN M ANSELL,
            PI   PIETER CULLIS,PETER SCHERRER,DAN SUITE DEBEYER PC   A61K9/00
            CC   Strandedness: Single;
```

```
           CC   Topology: Linear;
           FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Chlamydia sp."
                     /mol_type="genomic DNA"
                     /db_xref="taxon:35827"
ORIGIN

  Query Match            100.0%;  Score 15;  DB 6;  Length 15;
  Best Local Similarity  100.0%;  Pred. No. 1.2e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATGC 15
              |||||||||||||||
Db          1 GTGCTCCATTGATGC 15


RESULT 12
AR073978
LOCUS       AR073978                 20 bp    DNA     linear   PAT 28-AUG-2000
DEFINITION  Sequence 47 from patent US 5952229.
ACCESSION   AR073978
VERSION     AR073978.1  GI:10000738
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Monia,B.P. and Boggs,R.T.
  TITLE     Antisense oligonucleotide modulation of raf gene expression
  JOURNAL   Patent: US 5952229-A 47 14-SEP-1999;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match            100.0%;  Score 15;  DB 6;  Length 20;
  Best Local Similarity  100.0%;  Pred. No. 1.1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATGC 15
              |||||||||||||||
Db          5 GTGCTCCATTGATGC 19


RESULT 13
AR216002
LOCUS       AR216002                 20 bp    DNA     linear   PAT 25-SEP-2002
DEFINITION  Sequence 49 from patent US 6410518.
ACCESSION   AR216002
VERSION     AR216002.1  GI:23314290
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Monia,B.P.
  TITLE     Antisense oligonucleotide inhibition of raf gene expression
  JOURNAL   Patent: US 6410518-A 49 25-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match            100.0%;  Score 15;  DB 6;  Length 20;
  Best Local Similarity  100.0%;  Pred. No. 1.1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATGC 15
              |||||||||||||||
Db          5 GTGCTCCATTGATGC 19


RESULT 14
AR110776
LOCUS       AR110776                 25 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 2 from patent US 6126965.
ACCESSION   AR110776
VERSION     AR110776.1  GI:12827624
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Kasid,U., Gokhale,P., Dritschilo,A. and Rahman,A.
  TITLE     Liposomes containing oligonucleotides
  JOURNAL   Patent: US 6126965-A 2 03-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match            100.0%;  Score 15;  DB 6;  Length 25;
  Best Local Similarity  100.0%;  Pred. No. 1.1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATGC 15
              |||||||||||||||
Db          8 GTGCTCCATTGATGC 22


RESULT 15
AR310686
LOCUS       AR310686                 25 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 2 from patent US 6559129.
ACCESSION   AR310686
VERSION     AR310686.1  GI:31703830
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Kasid,U., Gokhale,P., Zhang,C., Dritschilo,A. and Rahman,A.
  TITLE     Cationic liposomal delivery system and therapeutic use thereof
  JOURNAL   Patent: US 6559129-A 2 06-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match            100.0%;  Score 15;  DB 6;  Length 25;
  Best Local Similarity  100.0%;  Pred. No. 1.1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATGC 15
              |||||||||||||||
Db          8 GTGCTCCATTGATGC 22


Search completed: June 21, 2005, 02:55:37
Job time : 1681 secs
```

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: June 20, 2005, 20:41:00 ; Search time 434 Seconds
(without alignments)
204.599 Million cell updates/sec

Title: US-10-075-994A-1
Perfect score: 15
Sequence: 1 gtgctccattgatgc 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	15	100.0	15	2	AAV54043	Aav54043 Human ant
	2	15	100.0	15	2	AAV99435	Aav99435 Antisense
	3	15	100.0	15	3	AAZ98661	Aaz98661 Human c-r
	4	15	100.0	15	6	AAD22797	Aad22797 Human c-r
	5	15	100.0	15	9	ACC58517	Acc58517 Oligonucl
	6	15	100.0	15	9	ADA24233	Ada24233 Human c-r
c	7	15	100.0	15	10	ADB97458	Adb97458 Sense (AT
	8	15	100.0	15	10	ADB97456	Adb97456 Antisense
	9	15	100.0	15	10	ADF82830	Adf82830 Immunosti
	10	15	100.0	15	12	ADE90171	Ade90171 Human c-r
	11	15	100.0	15	12	ADE39690	Ade39690 Oligonucl
	12	15	100.0	15	12	ADF32025	Adf32025 Antisense
	13	15	100.0	15	12	ADF42926	Adf42926 Methylate
	14	15	100.0	15	12	ADL70154	Adl70154 Oligonucl
	15	15	100.0	15	13	ADR88950	Adr88950 Anti c-ra
	16	15	100.0	20	2	AAT27527	Aat27527 Mouse/rat
	17	15	100.0	20	2	AAZ11557	Aaz11557 Mouse and
	18	15	100.0	20	3	AAA73535	Aaa73535 Mouse and
	19	15	100.0	20	6	AAD44760	Aad44760 Mouse and
	20	15	100.0	20	10	ADF09751	Adf09751 Mouse/rat
	21	15	100.0	20	10	ACD42120	Acd42120 Antisense
	22	15	100.0	25	10	ADB97457	Adb97457 Oligo use
c	23	15	100.0	165	6	ABQ97799	Abq97799 Mouse ES
c	24	15	100.0	478	9	ACH17231	Ach17231 Human adu
	25	15	100.0	597	12	ACH77604	Ach77604 Human gen
	26	15	100.0	968	13	ADR60510	Adr60510 Cotton cD
c	27	15	100.0	1038	10	ADF57946	Adf57946 Human pol
c	28	15	100.0	2524	10	ADB58074	Adb58074 Toxicity-
c	29	15	100.0	2524	10	ADB52556	Adb52556 Primary r
c	30	15	100.0	2975	10	AAD64080	Aad64080 DNA #1 re
c	31	15	100.0	2975	12	ADL16251	Adl16251 Raf cDNA.
c	32	15	100.0	2977	2	AAT30085	Aat30085 Human Raf
c	33	15	100.0	2977	2	AAT61894	Aat61894 Human raf
c	34	15	100.0	2977	2	AAV20439	Aav20439 Human c-r
c	35	15	100.0	2977	2	AAX99340	Aax99340 Human c-r
c	36	15	100.0	2977	2	AAX78137	Aax78137 Human c-R
c	37	15	100.0	2977	3	AAA48654	Aaa48654 Human c-r
c	38	15	100.0	2977	3	AAA73552	Aaa73552 Polynucle
c	39	15	100.0	2977	5	AAF75126	Aaf75126 Human c-R
c	40	15	100.0	2977	6	ABL69999	Abl69999 Pancreas
c	41	15	100.0	2977	6	ABL57050	Abl57050 Human pro
c	42	15	100.0	2977	6	ABK72300	Abk72300 Lymphona
c	43	15	100.0	2977	6	AAI68698	Aai68698 Human c-r
c	44	15	100.0	2977	6	AAD44819	Aad44819 Human raf
c	45	15	100.0	2977	10	ADF18639	Adf18639 Human raf

ALIGNMENTS

RESULT 1
AAV54043
ID AAV54043 standard; DNA; 15 BP.
XX
AC AAV54043;
XX
DT 02-DEC-1998 (first entry)
XX
DE Human antisense c-raf-1 oligodeoxyribonucleotide.
XX
KW Human; antisense; c-raf-1; oligodeoxyribonucleotide; ODN/oligo;
KW tumour tissue; cancer; radiation therapy; radiosensitise; antisense;
KW liposome carrier system; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1
FT /*tag= a
FT /note= "N-terminal base is phosphothioated"
FT modified_base 15
FT /*tag= b
FT /note= "C-terminal base is phosphothioated"
XX
PN WO9843095-A1.
XX
PD 01-OCT-1998.
XX
PF 19-MAR-1998; 98WO-US005303.
XX
PR 21-MAR-1997; 97US-0041192P.
PR 24-OCT-1997; 97US-00957327.
XX
PA (GEOU) UNIV GEORGETOWN.
XX
PI Kasid U, Gokhale P, Dritschilo A, Rahman A;
XX
DR WPI; 1998-532155/45.
XX
PT New cationic liposome composition containing raf oligodeoxynucleotide -
PT can be used to directly target tumour tissue and is useful in the
PT radiation therapy of cancers.
XX

```
PS   Claim 4; Page 21; 25pp; English.
XX
CC   This is the nucleotide sequence of the human antisense c-raf-1
CC   oligodeoxyribonucleotide (ODN/oligo), used in the method of the invention
CC   to directly target tumour tissue, and in cancer radiation therapy. The
CC   products can be used in a method of radiosensitising tumour tissue by
CC   addition of an antisense oligonucleotide of maximum 40 bases containing
CC   ODN/oligo. The liposome carrier system directly targets tumour tissue and
CC   has the potential for use in the radiation therapy of cancers
XX
SQ   Sequence 15 BP; 2 A; 4 C; 4 G; 5 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 15;  DB 2;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATGC 15
              |||||||||||||||
Db          1 GTGCTCCATTGATGC 15


RESULT 2
AAV99435
ID   AAV99435 standard; DNA; 15 BP.
XX
AC   AAV99435;
XX
DT   22-MAR-1999  (first entry)
XX
DE   Antisense oligonucleotide directed against c-raf-1 protein kinase gene.
XX
KW   Antisense oligonucleotide; human c-raf-1 protein kinase gene;
KW   phosphorothioate; phosphodiester; lipid-encapsulation; tumour;
KW   aberrant gene expression; treatment; inflammation; infection; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .15
FT                    /*tag=  a
FT                    /note= "phosphorothioate or phosphodiester bonds"
XX
PN   WO9851278-A2.
XX
PD   19-NOV-1998.
XX
PF   14-MAY-1998;   98WO-CA000485.
XX
PR   14-MAY-1997;   97US-00856374.
XX
PA   (INEX-) INEX PHARM CORP.
XX
PI   Semple SC,  Klimuk SK,  Harasym T,  Hope MJ,  Ansell SM,  Cullis P;
PI   Scherrer P,  Debeyer D;
XX
DR   WPI; 1999-045179/04.
XX
PT   Composition containing lipid-encapsulated therapeutic agent - useful,
PT   e.g. for delivering antisense molecules or ribozymes or treating diseases
PT   associated with aberrant gene expression.
XX
PS   Disclosure; Page 23; 98pp; English.
XX
CC   The present sequence represents an antisense oligonucleotide directed
CC   against the human c-raf-1 protein kinase gene. The oligonucleotide can
CC   have either phosphorothioate or phosphodiester bonds. The oligonucleotide
CC   is lipid-encapsulated using the method of the invention. A composition
CC   comprising lipid-encapsulated particles of a therapeutic agent, e.g.
CC   antisense oligonucleotides, is prepared by mixing at least 2 lipids with
CC   buffered aqueous solution of charged therapeutic agent to form an
CC   intermediate mixture of lipid-encapsulated particles, and changing the pH
CC   of the mixture to neutralise at least some of the external surface
CC   charges on the particles. One lipid has a (de)protonatable group with Ka
CC   such that the lipid is charged at a first pH but neutral at a second pH
CC   (particularly near physiological pH) and the buffer maintains this lipid
CC   in the charged form (i.e. cationic when the therapeutic agent is anionic
CC   in the buffer, or vice versa). The second lipid prevents particle
CC   aggregation during formation of the lipid-therapeutic agent particles.
CC   The composition is used to introduce therapeutic agents into cells, in
CC   vivo or in vitro, particularly to treat or prevent diseases associated
CC   with aberrant gene expression in mammals, specifically tumours,
CC   inflammation or infection
XX
SQ   Sequence 15 BP; 2 A; 4 C; 4 G; 5 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 15;  DB 2;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATGC 15
              |||||||||||||||
Db          1 GTGCTCCATTGATGC 15


RESULT 3
AAZ98661
ID   AAZ98661 standard; DNA; 15 BP.
XX
AC   AAZ98661;
XX
DT   05-JUN-2000  (first entry)
XX
DE   Human c-raf-1 PK therapeutic antisense oligonucleotide sequence ATG-AS.
XX
KW   Antisense oligonucleotide; phosphorothioate; inflammatory disease;
KW   tumour; gene therapy; aberrant gene expression; treatment;
KW   infectious disease; protein kinase C alpha; c-raf-1 protein kinase; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   misc_feature     1. .15
FT                    /*tag=  a
FT                    /note= "Optionally phosphorothioate internucleotide
FT                    linkages"
XX
PN   CA2271582-A1.
XX
PD   14-NOV-1999.
XX
PF   13-MAY-1999;   99CA-02271582.
XX
PR   14-MAY-1998;   98US-00078955.
XX
PA   (KLIM/) KLIMUK S K.
PA   (HARA/) HARASYM T.
PA   (HOPE/) HOPE M J.
PA   (ANSE/) ANSELL S M.
PA   (CULL/) CULLIS P R.
PA   (MOKW/) MOK W W K.
PA   (SCHE/) SCHERRER P.
PA   (SEMP/) SEMPLE S C.
XX
PI   Klimuk SK,  Harasym T,  Hope MJ,  Ansell SM,  Cullis PR,  Mok WWK;
PI   Scherrer P,  Semple SC;
XX
DR   WPI; 2000-225058/20.
XX
PT   A method for delivering antisense oligonucleotides to cells using lipid
PT   capsules comprising steric barrier lipids.
XX
PS   Example 5; Page 57; 99pp; English.
XX
CC   This sequence represents an antisense oligonucleotide sequence which has
CC   human c-raf-1 protein kinase as its target gene. The oligonucleotide is
```

```
CC   used in a method for delivering lipid encapsulated therapeutic agents
CC   (i.e antisense oligonucleotides) to mammals. The lipid capsule comprises
CC   steric barrier lipids that prevent particle aggregation during lipid
CC   nucleic acid formation. The method may be used for the delivery of
CC   therapeutic agents to mammalian cells. It is especially suitable for
CC   delivering nucleic acid molecules, and in particular antisense molecules
CC   which may be administered to down regulate the expression of aberrant
CC   genes. The aberrant gene may be ICAM-1, c-myc, c-myb, ras, raf, erb-B-2,
CC   PKC-alpha, IGF-1R, EGFR, VEGF and/or VEG-R-1. The method may be used for
CC   the treatment of tumours, inflammatory diseases and/or infectious
CC   diseases
XX
SQ   Sequence 15 BP; 2 A; 4 C; 4 G; 5 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 15;  DB 3;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATGC 15
              |||||||||||||||
Db          1 GTGCTCCATTGATGC 15


RESULT 4
AAD22797
ID   AAD22797 standard; DNA; 15 BP.
XX
AC   AAD22797;
XX
DT   26-FEB-2002  (first entry)
XX
DE   Human c-raf-1 protein kinase antisense oligonucleotide, ATG-AS.
XX
KW   Treatment; tumour; lipid-therapeutic agent particle; sphingomyelin;
KW   distearoylphosphatidylcholine; palmitoyloleoyl phophatidylcholine; DSPC;
KW   POPC; 1,2-dioleoyl-sn-3-phosphoethanolamine; cholesterol; SM; DOPE;
KW   inflammation; c-raf-1 protein kinase gene; human; infectious disease; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "Optionally phosphorothioate backbone"
FT
XX
PN   US6287591-B1.
XX
PD   11-SEP-2001.
XX
PF   14-MAY-1998;   98US-00078954.
XX
PR   14-MAY-1997;   97US-00856374.
XX
PA   (INEX-) INEX PHARM CORP.
XX
PI   Semple SC,  Klimuk SK,  Harasym T,  Hope MJ,  Ansell SM,  Cullis P;
PI   Scherrer P,  Debeyer D;
XX
DR   WPI; 2002-024658/03.
XX
PT   Composition useful for treatment of e.g. tumors comprises particles
PT   comprising lipid portion and a charged therapeutic agent.
XX
PS   Disclosure; Col 15-16; 48pp; English.
XX
CC   The invention relates to a composition useful for treatment of e.g.
CC   tumours. The composition comprises lipid-therapeutic agent particles
CC   comprising a lipid portion and a charged therapeutic agent which is
CC   encapsulated in the lipid portion. The lipid portion comprises a first
CC   lipid component selected from lipids containing a protonatable or
CC   deprotonatable (preferably protonatable) group that has a pKa such that
CC   the lipid is in charged form at a first pH and in neutral form at a
CC   second pH. The pKa of lipid component is from 4-11. The first lipid
CC   component is further selected such that the charged form is cationic when
CC   the therapeutic agent is anionic and vice versa; the second lipid
CC   component is selected from lipids that prevent particle aggregation
CC   during lipid-therapeutic agent particles formation and which exchange out
CC   the lipid particle at a rate greater than PEG-CerC20; third lipid
CC   component is a neutral lipid selected from distearoylphosphatidylcholine
CC   (DSPC), palmitoyloleoyl phophatidylcholine (POPC), 1,2-dioleoyl-sn-3-
CC   phosphoethanolamine (DOPE) or SM (sphingomyelin) and a fourth lipid
CC   component which is cholesterol. Compositions of the invention are used
CC   for treatment or prevention of a disease caused by aberrant expression of
CC   a gene preferably ICAM-1 (Intracellular adhesion molecule-1), c-myc, c-
CC   myb, ras, raf, erb-B-2, PKC-alpha (phosphokinase C-alpha), IGF-1R
CC   (insulin growth factor 1-receptor), bcl-2, EGFR (epidermal growth factor
CC   receptor), VEGF and VEGF-R-1 (vascular endothelial growth factor receptor
CC   1) in a mammal or by inflammations such as tumour or an infectious
CC   disease. The present sequence is an antisense oligonucleotide targetted
CC   to human c-raf-1 protein kinase gene
XX
SQ   Sequence 15 BP; 2 A; 4 C; 4 G; 5 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 15;  DB 6;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATGC 15
              |||||||||||||||
Db          1 GTGCTCCATTGATGC 15


RESULT 5
ACC58517
ID   ACC58517 standard; DNA; 15 BP.
XX
AC   ACC58517;
XX
DT   26-AUG-2003  (first entry)
XX
DE   Oligonucleotide ODN #25 (hC-Raf1).
XX
KW   Lipid nucleic acid; LNA; mucosal; vaccine; immunostimulant; human;
KW   C-Raf-s; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .15
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "OTHER= optional phosphorothioate nucleotides"
XX
PN   WO2003039595-A2.
XX
PD   15-MAY-2003.
XX
PF   07-NOV-2002; 2002WO-CA001717.
XX
PR   07-NOV-2001; 2001US-0337522P.
PR   10-MAY-2002; 2002US-0379343P.
XX
PA   (INEX-) INEX PHARM CORP.
XX
PI   Semple S,  Klimuk S,  Yuan Z;
XX
DR   WPI; 2003-493235/46.
XX
PT   Improved mucosal adjuvant useful in the preparation of vaccine for
PT   stimulating an immune response comprises a lipid-nucleic acid formulation
PT   containing a nucleic acid component encapsulated by a lipid.
XX
PS   Disclosure; Page 21; 71pp; English.
XX
CC   The present sequence is that of oligodeoxynucleotide ODN #25 (hC-Raf-1)
```

```
CC   for human C-Raf-s. It is an example of an ODN that can be used in lipid-
CC   nucleic acid (LNA) formulations of the invention comprising a lipid
CC   component and a nucleic acid component. The invention is based on the
CC   discovery that such LNA formulations associated with a target antigen
CC   stimulate enhanced mucosal immune responses, especially IgA production,
CC   directed to that target antigen in vivo as compared to the target antigen
CC   alone or mixed with free or unencapsulated forms of the ODN. Claimed
CC   improved mucosal vaccines comprise an LNA formulation with at least one
CC   antigen, the LNA formulation comprising a lipid component that
CC   encapsulates the nucleic acid component, with the lipid and nucleic acid
CC   components acting synergistically to stimulate antigen-specific IgG
CC   production in a mammal
XX
SQ   Sequence 15 BP; 2 A; 4 C; 4 G; 5 T; 0 U; 0 Other;

  Query Match            100.0%;  Score 15;  DB 9;  Length 15;
  Best Local Similarity  100.0%;  Pred. No. 1.1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATGC 15
              |||||||||||||||
Db          1 GTGCTCCATTGATGC 15


RESULT 6
ADA24233
ID   ADA24233 standard; DNA; 15 BP.
XX
AC   ADA24233;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human c-raf-1 protein kinase antisense oligonucleotide SEQ ID NO:16.
XX
KW   therapeutic oligonucleotide; double-stranded RNA; dsRNA; mobile protein;
KW   cytostatic; immunosuppressive; virucide; anti-HIV; antibacterial;
KW   cardiant; hyperproliferation; cancer; haematological; metastatic;
KW   autoimmune disease; infection; endocrine; neural; cardiovascular;
KW   pulmonary; reproductive system disorder; endocytosis; metabolic process;
KW   murine; intracellular adhesion molecule 1; ICAM-1;
KW   antisense oligonucleotide; phosphorothioate; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .15
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "optionally phosphorothioate backbone"
XX
PN   WO2003069306-A2.
XX
PD   21-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004323.
XX
PR   13-FEB-2002; 2002US-0356053P.
XX
PA   (MEDB-) MEDBRIDGE INC.
XX
PI   Xie D;
XX
DR   WPI; 2003-646491/61.
XX
PT   Treating diseases with oligonucleotides or interfering RNA, useful e.g.
PT   for cancer or autoimmune diseases, covalently coupled to mobile proteins,
PT   in vivo or in vitro.
XX
PS   Claim 128; Page 12; 42pp; English.
XX
CC   The present invention describes a method for treating a disease by
CC   administering: (a) a therapeutic oligonucleotide (TON) or double-stranded
CC   RNA (dsRNA) that includes a reactive group (RG) that can react with a
CC   mobile protein (MP) to form a covalent conjugate of TON/dsRNA and MP; or
CC   (b) TON or dsRNA already conjugated to MP through a covalent bond. Also
CC   described: (1) TON of 15-30 bases that includes (i) a part that binds to
CC   target RNA or DNA and (ii) RG; (2) TON of 15-30 bases that includes a
CC   part that binds to target RNA or DNA and is conjugated to MP through a
CC   covalent link; (3) dsRNA that includes RG; and (4) dsRNA that is
CC   conjugated to MP through a covalent link. TON have cytostatic,
CC   immunosuppressive, virucide, anti-HIV, antibacterial and cardiant
CC   activities. The method is used to treat, or prevent, hyperproliferation
CC   (particularly cancers, solid or haematological, including prevention of
CC   metastatic spread); autoimmune diseases; viral or bacterial infections;
CC   endocrine, neural, cardiovascular, pulmonary or reproductive system
CC   disorders. Also where TON or dsRNA are labelled, they can be used for
CC   diagnosis and monitoring of therapy. When linked to a mobile protein,
CC   TON/dsRNA have better cell entry (via endocytosis or other parts of the
CC   mobile protein metabolic process) and longer therapeutic life, increased
CC   from hours to weeks (the result of increased resistance to nuclease),
CC   without loss of affinity for the target. In many cases immune response to
CC   TON/dsRNA is also reduced, as is non-specific binding to endogenous
CC   proteins. The present sequence represents a human c-raf-1 antisense
CC   oligonucleotide, which is a specifically claimed TON from the present
CC   invention.
XX
SQ   Sequence 15 BP; 2 A; 4 C; 4 G; 5 T; 0 U; 0 Other;

  Query Match            100.0%;  Score 15;  DB 9;  Length 15;
  Best Local Similarity  100.0%;  Pred. No. 1.1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATGC 15
              |||||||||||||||
Db          1 GTGCTCCATTGATGC 15


RESULT 7
ADB97458/c
ID   ADB97458 standard; DNA; 15 BP.
XX
AC   ADB97458;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Sense (ATG-S) raf ODN oligodeoxyribonucleotide.
XX
KW   antisense; ATG-S; raf ODN; chemosensitisation; tumour tissue;
KW   chemotherapeutic agent; cationic liposome; cationic lipid;
KW   phosphatidylcholine; cholesterol; liposome;
KW   dimethyldioctadecyl ammonium bromide; DDAB;
KW   dimyristoyl trimethyl ammonium propane; DMTAP; phosphatidylcholine; PC;
KW   cholesterol; cancer; leukaemia; lymphoma; myeloma; carcinoma; sarcoma;
KW   combination therapy; pre-cancerous lesion; chemotherapy; ss.
XX
OS   Unidentified.
XX
PN   WO2003070221-A1.
XX
PD   28-AUG-2003.
XX
PF   14-FEB-2003; 2003WO-US004681.
XX
PR   15-FEB-2002; 2002US-00075994.
XX
PA   (GEOU ) UNIV GEORGETOWN.
PA   (NEOP-) NEOPHARM INC.
XX
PI   Kasid U,  Gokhale P,  Pei J,  Mewani R,  Ahmad I,  Drischilo A;
PI   Rahman A;
XX
DR   WPI; 2003-689738/65.
XX
PT   Chemosensitization of tumor tissue, useful for treating cancer, e.g.
PT   leukemia, lymphoma or myeloma, comprises administering a chemotherapeutic
```

PT agent and cationic liposomes containing oligonucleotides.
XX
PS Example 1; Page 18; 77pp; English.
XX
CC The invention relates to a novel method for the chemosensitisation of
CC tumour tissue, comprising administering a chemotherapeutic agent and a
CC composition comprising cationic liposomes consisting of cationic lipid,
CC phosphatidylcholine and cholesterol, where oligonucleotide(s) are
CC encapsulated within the liposome. The invention further relates to a
CC composition comprising liposomes consisting essentially of a cationic
CC lipid like dimethyldioctadecyl ammonium bromide (DDAB) or dimyristoyl
CC trimethyl ammonium propane (DMTAP), phosphatidylcholine (PC),
CC cholesterol, and containing the sequence 5'- GTGCTCCATTGATGC -3', where
CC only the terminal sequences are phosphorothioated. The method is useful
CC for chemosensitisation of a tumour tissue or cancer, including leukaemia,
CC lymphoma, myeloma, carcinoma or sarcoma. The combination therapy may be
CC used for any stage of cancer ranging from pre-cancerous lesions to cancer
CC of advanced stages. This polynucleotide sequence represents the sense
CC (ATG-S) raf ODN oligodeoxyribonucleotide, a cationic liposome of the
CC invention.
XX
SQ Sequence 15 BP; 5 A; 4 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 15; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCTCCATTGATGC 15
||||||||||||||||
Db 15 GTGCTCCATTGATGC 1

RESULT 8
ADB97456
ID ADB97456 standard; DNA; 15 BP.
XX
AC ADB97456;
XX
DT 04-DEC-2003 (first entry)
XX
DE Antisense (ATG-AS) raf ODN oligodeoxyribonucleotide.
XX
KW antisense; ATG-AS; raf ODN; chemosensitisation; tumour tissue;
KW chemotherapeutic agent; cationic liposome; cationic lipid;
KW phosphatidylcholine; cholesterol; liposome;
KW dimethyldioctadecyl ammonium bromide; DDAB;
KW dimyristoyl trimethyl ammonium propane; DMTAP; phosphatidylcholine; PC;
KW cholesterol; cancer; leukaemia; lymphoma; myeloma; carcinoma; sarcoma;
KW combination therapy; pre-cancerous lesion; chemotherapy; ss.
XX
OS Unidentified.
XX
PN WO2003070221-A1.
XX
PD 28-AUG-2003.
XX
PF 14-FEB-2003; 2003WO-US004681.
XX
PR 15-FEB-2002; 2002US-00075994.
XX
PA (GEOU) UNIV GEORGETOWN.
PA (NEOP-) NEOPHARM INC.
XX
PI Kasid U, Gokhale P, Pei J, Mewani R, Ahmad I, Drischilo A;
PI Rahman A;
XX
DR WPI; 2003-689738/65.
XX
PT Chemosensitization of tumor tissue, useful for treating cancer, e.g.
PT leukemia, lymphoma or myeloma, comprises administering a chemotherapeutic
PT agent and cationic liposomes containing oligonucleotides.
XX
PS Example 1; Page 18; 77pp; English.
XX
CC The invention relates to a novel method for the chemosensitisation of
CC tumour tissue, comprising administering a chemotherapeutic agent and a
CC composition comprising cationic liposomes consisting of cationic lipid,
CC phosphatidylcholine and cholesterol, where oligonucleotide(s) are
CC encapsulated within the liposome. The invention further relates to a
CC composition comprising liposomes consisting essentially of a cationic
CC lipid like dimethyldioctadecyl ammonium bromide (DDAB) or dimyristoyl
CC trimethyl ammonium propane (DMTAP), phosphatidylcholine (PC),
CC cholesterol, and containing the sequence 5'- GTGCTCCATTGATGC -3', where
CC only the terminal sequences are phosphorothioated. The method is useful
CC for chemosensitisation of a tumour tissue or cancer, including leukaemia,
CC lymphoma, myeloma, carcinoma or sarcoma. The combination therapy may be
CC used for any stage of cancer ranging from pre-cancerous lesions to cancer
CC of advanced stages. This polynucleotide sequence represents the antisense
CC (ATG-AS) raf ODN oligodeoxyribonucleotide, a cationic liposome of the
CC invention.
XX
SQ Sequence 15 BP; 2 A; 4 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 15; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCTCCATTGATGC 15
||||||||||||||||
Db 1 GTGCTCCATTGATGC 15

RESULT 9
ADF82830
ID ADF82830 standard; DNA; 15 BP.
XX
AC ADF82830;
XX
DT 26-FEB-2004 (first entry)
XX
DE Immunostimulant ODN25, component of lipid-nucleic acid vaccine.
XX
KW Immunostimulant; vaccine; lipid-nucleic acid; phosphorothioate; human;
KW C-Raf-s; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1. .15
FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER= optional phosphorothioate nucleotides"
XX
PN WO2003094829-A2.
XX
PD 20-NOV-2003.
XX
PF 12-MAY-2003; 2003WO-CA000680.
XX
PR 10-MAY-2002; 2002US-0379343P.
PR 07-NOV-2002; 2002US-00290545.
PR 12-MAR-2003; 2003US-0454298P.
XX
PA (INEX-) INEX PHARM CORP.
XX
PI Semple S, Chikh G, Hope MJ, Tam YK;
XX
DR WPI; 2003-903935/82.
XX
PT New pathogen vaccine having a lipid-nucleic acid formulation in
PT combination with at least one microbial antigen, useful for stimulating
PT enhanced responses against bacterial, viral and parasitic infections.
XX
PS Disclosure; SEQ ID NO 25; 138pp; English.
XX

```
CC   The present sequence is that of ODN25 (C-Raf-s) for human C-Raf-s. This
CC   is an immunostimulatory oligonucleotide that can be used in lipid-nucleic
CC   acid (LNA) vaccines of the invention. Claimed vaccines comprise an LNA
CC   formulation in combination with at least one microbial antigen, such as
CC   hepatitis B virus surface antigen. The lipid component of the LNA
CC   comprises at least one cationic lipid. The oligonucleotide component of
CC   the LNA preferably comprises at least one CpG dinucleotide, a methylated
CC   cytosine and a phosphorothioate backbone. The vaccine is capable of
CC   stimulating Th1 type humoral and cellular immune responses. An enhanced
CC   humoral response is demonstrated by a strong early peak of interferon-
CC   gamma production observed within hours of vaccine followed by a second
CC   stronger peak of interferon-gamma production observed several days later,
CC   correlated with antibody isotype switching.
XX
SQ   Sequence 15 BP; 2 A; 4 C; 4 G; 5 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 15;  DB 10;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATGC 15
              |||||||||||||||
Db          1 GTGCTCCATTGATGC 15


RESULT 10
ADE90171
ID   ADE90171 standard; DNA; 15 BP.
XX
AC   ADE90171;
XX
DT   12-FEB-2004  (first entry)
XX
DE   Human c-raf-1 protein kinase antisense oligonucleotide.
XX
KW   ss; lipid-encapsulated therapeutic agent particle;
KW   aberrant gene expression; intercellular adhesion molecule; ICAM-1; c-myc;
KW   c-myb; ras; raf; erb-B-2; protein kinase C; PKC-alpha;
KW   insulin-like growth factor; IGF-IR; epidermal growth factor receptor;
KW   EGFR; vascular endothelial growth factor; VEGF; VEGF-R-1; tumour;
KW   inflammation; infection; antisense; human.
XX
OS   Homo sapiens.
XX
PN   US2003129221-A1.
XX
PD   10-JUL-2003.
XX
PF   29-JUN-2001; 2001US-00895480.
XX
PR   14-MAY-1997;   97US-00856374.
PR   14-MAY-1998;   98US-00078954.
XX
PA   (SEMP/) SEMPLE S C.
PA   (KLIM/) KLIMUK S K.
PA   (HARA/) HARASYM T.
PA   (HOPE/) HOPE M J.
PA   (ANSE/) ANSELL S M.
PA   (CULL/) CULLIS P.
PA   (SCHE/) SCHERRER P.
PA   (DEBE/) DEBEYER D.
XX
PI   Semple SC,  Klimuk SK,  Harasym T,  Hope MJ,  Ansell SM,  Cullis P;
PI   Scherrer P,  Debeyer D;
XX
DR   WPI; 2004-031296/03.
XX
PT   Preparation of a composition comprising lipid-encapsulated therapeutic
PT   agent particles, useful for introducing a nucleic acid into a cell and
PT   for treating diseases characterized by aberrant gene expression.
XX
PS   Disclosure; SEQ ID NO 15; 52pp; English.
XX
CC   The invention relates to a method of preparation of a composition
CC   comprising lipid-encapsulated therapeutic agent particles. The
CC   composition is useful for introducing a nucleic acid into a cell and for
CC   treating diseases characterized by aberrant gene expression (especially
CC   intercellular adhesion molecule (ICAM)-1, c-myc, c-myb, ras, raf erb-B-2,
CC   protein kinase C (PKC)-alpha, insulin-like growth factor (IGF)-IR,
CC   epidermal growth factor receptor (EGFR), vascular endothelial growth
CC   factor (VEGF) or VEGF-R-1), e.g. tumours, inflammation or infection. The
CC   present sequence represents an antisense oligonucletide.
XX
SQ   Sequence 15 BP; 2 A; 4 C; 4 G; 5 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 15;  DB 12;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATGC 15
              |||||||||||||||
Db          1 GTGCTCCATTGATGC 15


RESULT 11
ADE39690
ID   ADE39690 standard; DNA; 15 BP.
XX
AC   ADE39690;
XX
DT   12-FEB-2004  (first entry)
XX
DE   Oligonucleotide ODN 25 (hC-Raf-1) SEQ ID NO:25.
XX
KW   cancer; vaccine; lipid-nucleic acid; LNA; tumour-associated antigen;
KW   Th-1 based immune response; cytostatic; gene therapy;
KW   tumour growth inhibition; tumour; human; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .15
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "optionally phosphorothioate linkages"
XX
PN   WO2003094828-A2.
XX
PD   20-NOV-2003.
XX
PF   12-MAY-2003; 2003WO-CA000679.
XX
PR   10-MAY-2002; 2002US-0379343P.
PR   07-NOV-2002; 2002US-00290545.
PR   04-APR-2003; 2003US-0460646P.
XX
PA   (INEX-) INEX PHARM CORP.
XX
PI   Tam YK,  Semple S,  Klimuk S,  Chikh G;
XX
DR   WPI; 2004-011992/01.
XX
PT   New cancer vaccine having a lipid-nucleic acid formulation in combination
PT   with at least one tumor-associated antigen, useful for stimulating
PT   enhanced responses against tumor-associated antigens and for inhibiting
PT   tumor growth.
XX
PS   Example 9; SEQ ID NO 25; 119pp; English.
XX
CC   The present invention describes a cancer vaccine (I), which comprises a
CC   lipid-nucleic acid (LNA) formulation in combination with at least one
CC   tumour-associated antigen that is mixed with or associated with the LNA
CC   formulation comprising a lipid component having at least one cationic
CC   lipid, and a nucleic acid component comprising at least one
CC   oligonucleotide, where the vaccine is capable of stimulating a Th-1 based
```

CC immune response in vivo to the at least one tumour-associated antigen.
CC (I) has cytostatic activity, and can be used in vaccines, and in gene
CC therapy. The methods and compositions of the present invention can be
CC used for stimulating enhanced responses against tumour-associated
CC antigens and for inhibiting tumour growth. The present sequence
CC represents an oligonucleotide which is used in the exemplification of the
CC present invention.
XX
SQ Sequence 15 BP; 2 A; 4 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 15; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCTCCATTGATGC 15
|||||||||||||||
Db 1 GTGCTCCATTGATGC 15

RESULT 12
ADF32025
ID ADF32025 standard; DNA; 15 BP.
XX
AC ADF32025;
XX
DT 26-FEB-2004 (first entry)
XX
DE Antisense oligonucleotide of the invention.
XX
KW platelet; oligonucleotide; Thrombolytic; thrombocytosis; ss.
XX
OS Synthetic.
XX
PN WO2003099213-A2.
XX
PD 04-DEC-2003.
XX
PF 19-MAY-2003; 2003WO-US015922.
XX
PR 20-MAY-2002; 2002US-0382411P.
XX
PA (NEOP-) NEOPHARM INC.
XX
PI Gately ST;
XX
DR WPI; 2004-035033/03.
XX
PT Reducing the platelet count in a patient, useful for treating
PT thrombocytosis, comprises administering antisense oligonucleotides
PT inhibiting raf-1 gene with an agent that enhances penetration of the
PT oligonucleotide into cells.
XX
PS Example 1; SEQ ID NO 1; 14pp; English.
XX
CC The present invention relates to reducing the platelet count in a patient
CC comprises preparing a formulation of an oligonucleotide with an agent
CC that enhances penetration of the oligonucleotide into cells, and
CC administering the formulation to a patient having an elevated platelet
CC count. The oligonucleotide is useful for preparing a medicament for
CC reducing the platelet count in a patient, particularly for treating
CC thrombocytosis. The present sequence represents an oligonucleotide of the
CC invention.
XX
SQ Sequence 15 BP; 2 A; 4 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 15; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCTCCATTGATGC 15
|||||||||||||||
Db 1 GTGCTCCATTGATGC 15

RESULT 13
ADF42926
ID ADF42926 standard; DNA; 15 BP.
XX
AC ADF42926;
XX
DT 11-MAR-2004 (first entry)
XX
DE Methylated immunostimulatory oligonucleotide ODN 25 SEQ ID NO:25.
XX
KW lipid-methylated nucleic acid formulation; immune response;
KW lipid-nucleic acid; vaccine; immunostimulant; cytostatic;
KW antiinflammatory; antiarthritic; gene therapy; cancer; inflammation;
KW arthritis; immunodeficiency disorder;
KW methylated immunostimulatory oligonucleotide; ss.
XX
OS Synthetic.
XX
PN WO2003094963-A2.
XX
PD 20-NOV-2003.
XX
PF 12-MAY-2003; 2003WO-CA000678.
XX
PR 10-MAY-2002; 2002US-0379343P.
PR 07-NOV-2002; 2002US-00290545.
PR 04-APR-2003; 2003US-0460646P.
XX
PA (INEX-) INEX PHARM CORP.
XX
PI Tam YK, Semple S, Klimuk S, Chikh G;
XX
DR WPI; 2004-142698/14.
XX
PT Lipid-methylated nucleic acid formulation for stimulating an immune
PT response in an animal comprises a lipid component and a nucleic acid
PT component comprising a methylated nucleic acid sequence.
XX
PS Disclosure; SEQ ID NO 25; 102pp; English.
XX
CC The present invention describes a lipid-methylated nucleic acid
CC formulation for stimulating an immune response in an animal, comprising a
CC lipid component and a nucleic acid component which is a methylated
CC nucleic acid sequence. Also described: (1) an adjuvant comprising a lipid
CC -nucleic acid (LNA) formulation; (2) a vaccine comprising the LNA
CC formulation in combination with at least one target antigen; (3)
CC stimulating an enhanced host immune response to antigenic stimulation,
CC comprising administering to the host the LNA formulation; (4) stimulating
CC host dendritic cells in vivo, comprising contacting at least one
CC dendritic cell with the lipid-methylated nucleic acid formulation to a
CC host; and (5) simultaneously delivering antigenic and adjuvant immune
CC stimulation to antigen presenting cells, comprising the administration of
CC the LNA formulation associated with a target antigen. The lipid-
CC methylation nucleic acid formulation has immunostimulant, cytostatic,
CC antiinflammatory and antiarthritic activities, and can be used in
CC vaccines, and in gene therapy. The formulation and methods are useful in
CC stimulating a host's immune response to antigenic stimulation, or in
CC activating and/or expanding dendritic cell populations in response to
CC antigenic stimulation. They may be used for treating cancer,
CC inflammation, arthritis or immunodeficiency disorders. The present
CC sequence represents a methylated immunostimulatory oligonucleotide given
CC in the exemplification of the present invention.
XX
SQ Sequence 15 BP; 2 A; 4 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 15; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCTCCATTGATGC 15
|||||||||||||||
Db 1 GTGCTCCATTGATGC 15

```
RESULT 14
ADL70154
ID   ADL70154 standard; DNA; 15 BP.
XX
AC   ADL70154;
XX
DT   20-MAY-2004  (first entry)
XX
DE   Oligonucleotide antisense to raf.
XX
KW   Raf; antisense; liposome; drug delivery; cytostatic; ss.
XX
OS   Synthetic.
XX
PN   WO2004017944-A1.
XX
PD   04-MAR-2004.
XX
PF   13-AUG-2003; 2003WO-US025293.
XX
PR   23-AUG-2002; 2002US-0405378P.
XX
PA   (NEOP-) NEOPHARM INC.
XX
PI   Zhang J,  Ahmad I;
XX
DR   WPI; 2004-257219/24.
XX
PT   Treatment of cellular proliferative disease e.g. cancer involves
PT   administration of a composition comprising liposomal gemcitabine and
PT   negatively charged phospholipid.
XX
PS   Disclosure; SEQ ID NO 1; 25pp; English.
XX
CC   The present sequence is that of an antisense oligonucleotide to raf. The
CC   invention relates to novel gemcitabine compositions and their use in
CC   treating proliferative diseases such as cancer, particularly in mammals,
CC   especially in humans. The compositions include liposome-entrapped
CC   gemcitabine. The cancer is especially lymphoma, ovarian cancer, breast
CC   cancer, pancreatic cancer, lung cancer or colon cancer. The liposomal
CC   gemcitabine compositions can be used in conjunction with secondary
CC   therapeutic agents including antineoplastic, antifungal and antibiotic
CC   agents as well as antisense oligonucleotides, especially an antisense
CC   oligonucleotide to raf (claimed).
XX
SQ   Sequence 15 BP; 2 A; 4 C; 4 G; 5 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 15;  DB 12;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATGC 15
              |||||||||||||||
Db          1 GTGCTCCATTGATGC 15


RESULT 15
ADR88950
ID   ADR88950 standard; DNA; 15 BP.
XX
AC   ADR88950;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Anti c-raf-1 oligonucleotide.
XX
KW   C-raf-1; liposomal; antineoplastic; cytostatic; cancer; antisense; ss.
XX
OS   Synthetic.
XX
PN   WO2004071466-A2.
XX
PD   26-AUG-2004.
XX
PF   11-FEB-2004; 2004WO-US004555.
XX
PR   11-FEB-2003; 2003US-0446895P.
XX
PA   (NEOP-) NEOPHARM INC.
XX
PI   Bhamidipati S,  Ahmad Z,  Ahmad I;
XX
DR   WPI; 2004-635030/61.
XX
PT   Preparation of liposomal composition used for treating e.g. cancer
PT   involves dissolving lipid fraction in water miscible organic solvent and
PT   mixing solvent solution with aqueous solution.
XX
PS   Disclosure; Page 6; 27pp; English.
XX
CC   The invention relates to the preparation of a liposomal composition. The
CC   method involves: dissolving a lipid fraction in a water-miscible organic
CC   solvent; and mixing the water-miscible organic solvent solution
CC   comprising the lipid fraction with an aqueous solution under conditions
CC   to form a bulk liposomal composition. The method further involves adding
CC   at least one active principal to the water-miscible organic solvent prior
CC   to the addition of the lipid fraction, or to the aqueous solution prior,
CC   during or after the step (b), size-reducing the bulk liposomal
CC   composition to obtain a size-reduced liposomal composition, freeing the
CC   liposomal composition of the water-miscible organic solvent by
CC   diafiltration using a tangential flow filtration process and sterile
CC   filtration, sterile-filtering the liposomal composition and freeze-drying
CC   the liposomal preparation. Step (b) involves adding the water-miscible
CC   organic solvent solution to the aqueous solution while mixing and mixing
CC   of solution following addition of water-miscible solvent comprising the
CC   lipid fraction to the aqueous solution while cooling. The active
CC   principal comprises at least one antineoplastic or antifungal agent
CC   (preferably taxane, camptothecin or their derivatives, especially
CC   paclitaxel or docetaxel). The composition is used for the treatment of
CC   disease e.g. cancer. The composition eliminates the disease or its
CC   symptoms, need not completely eradicate the effects of the disease,
CC   reduces the severity of a disease, infection or reduction in the rate by
CC   which a disease progresses within a patient. The method permits the
CC   production of liposomal formulation on a commercial scale. The present
CC   sequence represents an antisense oligonucleotide specific for c-raf-1,
CC   that can be used as an active principal.
XX
SQ   Sequence 15 BP; 2 A; 4 C; 4 G; 5 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 15;  DB 13;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCTCCATTGATGC 15
              |||||||||||||||
Db          1 GTGCTCCATTGATGC 15


Search completed: June 21, 2005, 02:27:28
Job time : 438 secs
```